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pregnancy-specific	probable exported	cell wall-binding	plastid-lipid-asso	probable membrane	hypothetical prote	molybdenum formylm	Ig heavy chain pre	hypothetical prote	Ig kappa chain pre	Ig heavy chain V r

ALIGNMENTS

junctional adhesion molecule precursor - human

N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11

C;Species: Homo sapiens (man)

C;Date: 27-Oct-195 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: A59406; S56749

R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K

J. Immunol. 163, 553-557, 1999

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A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:g5326797; PIDN:AAD42050.1 R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E. Biochem. J. 310, 155-162, 1995 Biochem. J. 310, 155-162, 1995 A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking A;Reference number: S56749; MUID:95374438; PMID:7646439 A;Accession: S56749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma A;Reference number: A59406; MUID:99323940; PMID:10395639 A;Accession: A59406
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A; Residues: 1-299 < OZA>
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Matches 65
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224
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                                                                                                                                              175 YIWYK----QQTN------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
                                                                                                                                                                                               112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEODGSPPSE
                                                                                                                                                                                                                                              116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                  63 ----KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV
                                                                                                                                                                                                                                                                                                                                                                                               17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----
                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                              SDIVK 227
SNAVR 228
                                                                                                                                                                                                                                                                                                                                              GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV
                                                                                                  YTWFKDGI VMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 178.5; DB 2; llarity 26.5%; Pred. No. 3.5e-06; Conservative 36; Mismatches 93;
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RESULT

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elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May
C;Accession: 138346
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of A;Reference number: A57430; MUID:96026330; PN
A;Accession: 138346
A;Status: preliminary; translated from GB/EME
                                                                                                                                                                    coxsackie- and adenovirus receptor - bovine
c;Species: Bos prinigenius taurus (cattle)
c;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C;Accession: JC7780
R;Thoelen, I; Keyaerts, E; Lindberg, M; Van Ranst, M.
Biochem, Biophys. Res. Commun. 288, 805-808, 2001
A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenova; Reference number: JC7780
A;Reference number: JC7780
A;Contents: Liver
A;Accession: JC7780
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A; Status: preiim...
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
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                                                           A; Molecule type: mRNA
A; Residues: 1-365 <THO>
A; Cresterences: UNIPROT: QBWMV3; GB: AY033651
C; Comment: This protein serves as the primary as
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;Map position: 2q31-2q31
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Conservative 56;
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Pred. No. 0.00025;
56; Mismatches 169;
     Score 170;
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A;Title: Dtrk, a Drosophila
A;Reference number: S19247;
A;Accession: S19247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;690-1028/Domain: protein kinase homology <KIN>F;698-706/Region: protein kinase ATP-binding mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: FlyBase:Tk48D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1033 <PUL>
A;Cross-references: UNIPROT:Q24327; EMBL:X63453; NID:g7883; PIDN:CAA45053.1; PID:g7884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Pulido, D.; Campuzano, EMBO J. 11, 391-404, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Pulido,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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es 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      22 ILEVPES---VTGPWKGDVNLPC----TYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQ----GM
MTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIML
                                               RFRFLENGTLEIRNVQVEDEGSYGCTIGNSAGLKRED--VQLVVK-------
                                                                                                                                                                                 VQKLSVSK--PTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYK-----QQTNNQE 186
                                                                                                                                                                                                                              DHVE-----VDANGTLIFRNVNSEHRGNYTCLATNSQGQINATV--AINVVV
                                                                                                                                                                                                                                                                           DHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVGSDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RISLQCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLSDIGTYQCKVKKAPGVGNK-----KIQLTVLVKP-----SGIRCYVDGSEEIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -IEWLLSPADNOKVDQVIILY---SGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKWLVQRGS----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQV
                                                                                      PIKVATLSTLLEKPAVIADSGSYFCTAKGOVGSEQHSDIVKFVVKDSSKLLKTKTEAPTT
                                                                                                                                     TPKFSVPPVGPIETSEQG-----TVVMHCQAIGDPKPTIQWDKDLKYLSENNTDRE
                                                                                                                                                                                                                                                                                                                           ILEVIEQLKFVPQPTSKNLELDAVVAKVHCKAQGTPTPQVQWV--RDGENTTL-----P
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                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 144.5; DB 2;
Pred. No. 0.0067;
3; Mismatches 141;
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0; Mismatches 1
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A;Note: sequence;extracted from NCBI backbone (NCBIN:135151, NCBIP:135153)
R;8h1sh1do, E.; Bmori, Y.; Saigo, K.
FEBS Lett. 289, 435-238, 1991
A;Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila A;Reference numbér: S17552; MUID:92008631; PMID:1915852
A;Accession: S18010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text C,Accession: B49120; 518010
R,Shishido, E.; Higashijima, S.; Emori, Y.; Saigo, K. Development 117, 751-761, 1993
A,Title: Two FGF1-receptor homologues of Drosophila: one A,Reference number: A49120; MUID:93321617; PMID:8330538
A,Accession: B49120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: PlyBase:btl; dtk2
A;Cross-references: FlyBase:FBgn0005592
C;Superfamily: protein kinase homology
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A; Residues: 1-1052 <SHI>
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                                                                                                                                                                                                                                                           VVRDKITELRVQKLSVSKPTVTTGSGYGPTVPQGMRISLQCQARGS---PPISYIWYKQQ 181
                                                                                                                                                                                                                                                                                                                              VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ 124
                                                                                                                                                                                                                                                                                                                                                                                                DTYGRPILE-----VPESVTGPWKGDVNLPCT-YDP-LOGYTQVLVKWLVQRGSDP
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                PVF 396
                                                                                   ASYVDLYSPSDTTTVRTTT--TTTVASPIPTASTGEDNDD---DVENPAADASGGVGP--
                                                                                                                    SDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSL 282
                                                                                                                                                       ADNIDDLLQRLREQSQLPVDVTRLITRMDEPQVLRLGNVLMEDGGWYICIAENQVGRTVA
                                                                                                                                                                                                                                                                                              -----HIDTQILGGRGRIKLK---RWSLTVGQLQPEDAGSYHCELCVE----QD
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 143.5; DB 2; 23.4%; Pred. No. 0.0082; tive 44; Mismatches 119;
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A;Molecule type: mRNA
A;Residues: 1-3707 <NO>
A;Cross-references: UNIPROT:(005793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002
A;Cross-references: UNIPROT: (005793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002
R;Moonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass
R;Diol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
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A;Residues: 1870-2600 <NO3>
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
A;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.

Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a A;Reference number: $66460; MUID:95377282; PMID:7649154
A;Reference number: $66460; MUID:95377282; PMID:7649154
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C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
C;Accession: S18252; A31917; B31917; S64460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, B.; Sasaki, M.; Yamada, J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;3270-3423/Domain: laminin G repeat homology <LG2>F;3464-3492/Domain: EGF homology <EGF7>
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A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 940-1601 < NO2>
A; Cross-references: GB: J04054;
A; Accession: B31917
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A;Accession: S18252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.6%;
Local Similarity 25.1%;
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IPGGSTPTVQVTPQLETRNIGAS
                                                                                                                                                                                                                                                                                                                                                             EATVV----LHVESPP-----YATTIPEHTSAQPGNLVQLQCLAHGTPPLTYQW--SLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIVDTGTVAPGTPQVQVEES-----ELTLEA----
                                                                                                                                                                                                                                                               NNQEPIKVATLSTLL-FKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KITELRVQKLSVSKPTVTTGSGYGFTVPQ-----GMRISLQCQARGSPPISYIWYKQQT
                                                                                     ----EAPTTMTYPLKATSTVKQS
                                                                                                                                                                          GGVLPEKAVVRNQLLRLEPTVPEDSGRYRCQVSNRVGSAE - - AFAQVLVQGSSSNLPDTS
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Pred. No. 0.083
31; Mismatches
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F;598-965/Domain: protein kinase homology <KIN's F;606-614/Region: protein kinase ATP-binding motif F;45,89,103,215,230,292,307,354,371,468,479/Binding site: F;54-100,149-190,235-291,436-508/Disulfide bonds: #status F;634/Active site: Lys #status predicted F;657/Binding site: phosphate (Tyr) (covalent) (by autombr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Claesson-Welsh, L., Eriksson, A.; Moren, A.; Severinsson, L.; Mol. Cell. Biol. 8, 3476-3486, 1988

A;Title: cDNA cloning and expression of a human platelet-derived A;Reference number: A31195; MUID:89096941; PMID:2850496

A;Mcleenlo L., A31195
                                                                                                                                                                                                                                                    F;47-102/Domain: immunoglobulin homology <IMM1>
F;142-192/Domain: immunoglobulin homology <IMM2>
F;142-192/Domain: immunoglobulin homology <IMM2>
F;228-293/Domain: immunoglobulin homology <IMM3>
F;429-510/Domain: immunoglobulin homology <IMM4>
F;532-555/Domain: transmembrane #status predicted <
F;556-1106/Domain: intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120710; OMIM:173410
A;Map position: 5q31-5q32
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer. F;1-32/Domain: signal sequence #status predicted <STG>F;1-32/Domain: signal sequence #status predicted <STG>F;33-31106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>F;33-531/Domain: extracellular #status predicted <EXT>
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A;Residues: 1047-1106 <RO3>
C;Comment: The extracellular domain is
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A;Cross-references: GB:M21616; NID:g189729; PIDN:AAA36427.1; PID:g189730
A;Cross-references: GB:M21616; NID:g189729; PIDN:AAA36427.1; PID:g189730
A;Parcanen, J:, Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: A38268
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C;Date: 31-Dec-1992 #text change 09-Jul-2004
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A28206; A31195; A38268; A31925; B31925; C31925
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth
A;Reference number: A28206; MUID:88217915; PMID:2835772
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A; Residues: 901-932 < RO2>
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A;Title: Tandem linkage of human CSF-1 receptor (c-fms)
A;Reference number: A90908; MUID:89028677; PMID:2846185
A;Accession: A31925
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A;Residues: 676-727 <ROB>
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A; Residues: 1-1106 < GRO>
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R;Roberts, W.M.; Look, A.T.; Roussel, M.F.; Sherr, C.J.
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Best Local
Similarity
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19.7%;
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Score 139; DB 1;
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L.; Ek, B.; Oestman, A.; Bet
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---QEFEVVSTL 495
                                     CIGQEYQIIAQI
                                                                                                                           NDSGE-TMRVA-----IFASGC---
                                                                                                                                                                NVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLELSESHP---
                                                                                                                                                                                                          VVFTMAYI - - - - MLCRKTSQQEH - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIW-YKQQTNNQ--EPIKVA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----FEDRSYICKTTIGD----REVDSDAYY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFSGI
                                                                                                                                                                                                                                                    TLQFAELHRSRTLQVVFEAYPPPTVLWFKD-NRTLGDSSAGE----
                                                                                                                                                                                                                                                                                            TTMTYPLKATSTVKQSWD-----WTTDMDGYLGETSAGPGKSLPVFAIILIISLCCM 296
                                                                               -DSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNSSEEESQLETNVTYWEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                       SDEPTSQNLGNNYSDEP
                                                                                                                                                                                                            -VYEAARAHAREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162;
                                                                                                                                                                                                                                                      ---- IALSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VYRLQ
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                                                                                     486
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                                                                                                                                                                     427
                                                                                                                                                                                                                                                      370
                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
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A;Title: A novel domain sequence of connectin localized A;Reference number: PN0568; MUID:93356802; PMID:8352787 A;Accession: PN0568 Biochem. Biophys. Res. Commun. 194, A; Title: A novel domain sequence of A; Reference number of the sequence o A; Experimental source: skeletal muscle C; Comment: This protein A;Residues: 1-1323 <MAR>
A;Cross-references: UNIPROT:Q08476; DDBJ:D16541; NID:g391629; A; Molecule type: mRNA C; Accession: C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: PN0568 N;Alternate names: Cn3B protein
Connectificate names: Cn3B protein
Connectification of the connectific connectin 3B -Matches Query Match ocal Similarity This protein string-like single molecule spans from the 61; chicken (fragment) Conservative 6.6%; H.; Kawamura, Y.; Kanzawa, N.; Nakauchi, Y.; Kimura, Score 138.5; DE Pred. No. 0.026; Mismatches DB 2; 117; Indels Length 1323; at the PID:d1004495; PID:g391630 1 band of skeletal 69; N to the M

muscle s.;

203

VAGTPEMIVSWYKGDTKLRGTATVKMHFKNQV---ATLVFSQVDSDDSGEYICKVENTVG

259

-----RLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP

-VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISY 175

GLPVTFDCGIAGSEPIEV

307

SWFKDNVRVKEDYNVHTSFIDNVAILQILKTDKSLMGQYTCTASNAIGT-

357

TWYKQQTNNQEPIKVAT--LSTLLFKPAVIADS---GSYFCTAKGQVGSEQHSDIVKFVV 230

79

QAK----

121

143

22

ILEVPESV---TGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQ

ILEIPNSKLEDQGQYSCHIENDSGQDNCHGAITILEPPYFVTPLEPVQVTVGDSASLQCQ

202

78

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A;Reference number: Z16469
A;Accession: T08678
A;Molecule type: mRNA
A;Residues: 1-584 <WAM>
A;Cross-references: UNIPROT:Q9Y3Y8; EMBL:AL049946
A;Experimental source: fetal brain; clone DKFZp564
C;Genetics:
A;Note: DKFZp564I1922.1
                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08678
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
T08678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connectin/titin - chicken (fragment)
(;Species: Gallus gallus (chicken)
(;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
(;Accession: T4263)
R;Yajima, H.; Ohreuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; I
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin:
A;Reference number: Z22221; MUID:96254045; PMID:8660363
A;Accession: T42633
A;Accession: T4263
A;Molecule type: mRNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:g1513029; PIDN:BAA11908.1; PID:g1:A;Experimental source: breast muscle
C;Keywords: skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein DKFZp564I1922.1 - C;Species: Homo sapiens (man)
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                                                                                     Query Match
Best Local S
Matches 53
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3955 VAGTPEMIVSWYKGDTKLRGTATVKMHFKNQV---ATLVFSQVDSDDSGEYICKVENTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                 15
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                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAK-----YQG------RLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
                                                   GDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSGKLVLTEGKTPPFFDTPI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWFKDNVRVKEDYNVHTSFIDNVAILQILKTDKSLMGQYTCTASNAIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IWYKQQTNNQEPIKVAT--LSTLLFKPAVIADS---GSYFCTAKGQVGSEQHSDIVKFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATSSSLLTVQERKLPPSFTRKLRDVHETV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGNQ-----VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILEIPNSKLEDQGQYSCHIENDSGQDNCHGAITILEPPYFVTPLEPVQVTVGDSASLQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILEVPESV---TGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQ
                 GDLKVDCV---ATGLPNPEISWSLPDGSLVNSFMQSDDSGGRTKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSGKLVLTEGKTPPFFDTPI----
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                                                                                       Conservative
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                                                                                                        6.5%;
                                                                                     Score 136; DB 2;
Pred. No. 0.014;
7; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 138.5; D
Pred. No. 0.11;
                                                                                                                                                                                               clone DKFZp564I1922
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                                                                                                                                                                                                                                                                                                                                                                                                  human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TPVDGIIGESA 4141
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                                                                                       99;
                                                                                                                       Length
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                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                  -YVVFN
                                                                                       Gaps
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                 61
                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
T20992
             hemicentin precursor - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 C;Accession: T43290; T20993; T24734 R;Vogel, B.E.; Hedgecock, E.M.
                                                                                                          RESULT
T43290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T20992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
B.E.; He
                                                                                                                                                                                                                                                        2897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
Library,
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
A;Residues: 1-5175 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.
A;Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F15G9.4a - Caenorhabditis eleg
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #Bequence_revision 15-Oct-1999
C;Accession: T20992; T24733
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: Z19929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q8I0L3;
A;Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                        2796 HAHDESVONGVITSKYAANEKTLNVTNIQLDDEGFYYC----TAVNEAGITKKFFKLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 HIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVPYGDVVTVACEAKGEPMPKVTWLSPTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNY
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                                                                                                                                  SDEVDIIGSTLVIDNPQKEVEGRYTCIAENKAGRSEKDMMVEVLLPPKLSKEWINVEVQA
                                                                                                                                                                                                      PIKVATL-STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVV--KDSSKLLKTKTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCTAKGQVGSEQH----
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GDPLTLECPIEDTSGVHITWSRQFGKDGQL 2986
                                                               --PTTMTYPLKATSTVKQSWDWTTDMDGYL
                                                                                                                                                                                                                                                                                                                                     -----QKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNNQE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCLVRNSAGEDRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEGIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4%; Score 133.5;
22.9%; Pred. No. 0.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                            -----YPIILGKRLTLDCSATGTPPPTILFMKDGKRLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: Z47068; PIDN: CAA87335.1; GSPDB: GN00028; CESP: F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NOVGKÓ---EMRVRVKVVTAPATIRNKTCLAV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
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June

1998

#text_change

09-Jul-2004

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A; Note:
C; Superf
                                                                                                                                                                                                                                                                                       RESULT 13
(42632
(42632
cell adhesion molecule apCAM (clone dl2) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C42632
R;Mayford, M; Barzilai, A; Keller, F.; Schacher, S; Kandel, E.R.
                                                                                                                                                                                                         Science 256, 638-644, 1392
A;Title: Modulation of an NCAM-related adhesion molecula
A:Reference number: A42632; MUID:92263095; PMID:1585176
                                                                                                                                            A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Molecule type: AAX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-5198 <WIZ>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.
A;Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sulston, J.
submitted to the EMBL Data
A;Reference number: Z19355
A;Accession: T20993
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                                                                                                A; Experimental source: CNS
                                                                                                                     A; Cross-references: UNIPROT: 09TWA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kershaw, J. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-5198 <WIL>
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.
A;Experimental source: clone F15G9
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A; Residues: 1-5198 < VOG>
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Best Local S
Matches 48
                                                     Superfamily:
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         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IETPYFLDQQKL------YPIILGKRLTLDCSATGTPPPTILFMKDGKRLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAHDESVONGVITSKYAANEKTLNVTNIQLDDEGFYYC----TAVNEAGITKKFFKLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDPLTLECPIEDTSGVHITWSRQFGKDGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PTTMTYPLKATSTVKQSWDWTTDMDGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIKVATL-STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVV--KDSSKLLKTKTEA 243
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                                                   acted from NCBI backbone cell adhesion molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%;
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         Score 132.5;
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Pred. No. 0.37;
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                                                                      RESULT 15
A42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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RESULT 14
B42632
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A;Title: Modulation of an NCAM-related adhesion molecule A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: B42632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared A;Molecule type: nucleic acid A;Residues: 1-812 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell adhesion molecule apCAM (clone d15) - California sea hare C;Species: Aplysia californica (California sea hare) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_chang
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les 54; Conserv
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                                                                 TVQYKPNFDTDFKEREFFGWRGHKANLTCQANANPVATIEWYMPDAENPDDYSKAVRIPN
                                                                                                                                     GIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL
                                EAPTIMIYPLKAISTVKQSWD
                                                                                                                                                                                                                                                                         KVGDEVKITCQATGVPPPTYQFKKGDVMVTDEMVNNGVLTINPLKTTDQATYTCIATNKG
                                                                                                                                                                                                                                                                                                         EMDDRSHYTCEV-----TWOTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMDDRSHYTCEV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG
                                                                                                                                                                   -----YKQQTNNQEPIKVATLST-LLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKF
                                                                                                                                                                                                       -GFAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAKGDPEPSVIWKKDGPQSASTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAPYTI - - - - - - NMLQKWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YKQQTNNQEPIKVATLST-LLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GFAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAKGDPEPSVIWKKDGPQSASTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
38-644, 1992
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-NMLQKWD
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 132.5; DB
Pred. No. 0.041;
1; Mismatches
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                                262
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                                                                                                                                                                                                                                         -QGMRISLQCQARGSPPISYIW------
                                                                                                                                                                                                                                                                                                                                                                                                             fibronectin type
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C;Accession: A42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: A42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-932 <MAY>
A;Cross-references: UNIPROT:Q9TWA6
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;Note: sequence extracted from NCBI backbone (NCBIP:101342)
;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hohiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J. W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Jones S.J., Marra M.A.;
Randing R.M., Marra M.A.;
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TISSUE-Brain;

Director MGC Project;

Director MGC Project;

Submitted (JUL-2001) to the EME
Submitted (JUL-2001) to the EME
EMBL; AJ13250; CAB51536.1; -.

EMBL; BC010525; AAH10525.1; -.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR007110; Ig-c2.

Pfam; PF00047; ig; 1.

SMART; SM00408; IGc2; 1.

SMART; SM00408; IGc2; 1.

PROSITE; P850835; IG_LIKE; 2.

Signal.

SIGNAL
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Q9Y279;
Q9Y279;
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
25-OCT-2004 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=20461865; PubMed=11004523; DOI=10.1016/S0167-4781(00)00131-7;
Langnaese K., Colleaux L., Kloos D.U., Fontes M., Wieacker P.;
Langnaese K., Colleaux L., Kloos D.U., Fontes M., Wieacker P.;
"Cloning of Z39Ig, a novel gene with immunoglobulin-like domains
located on human chromosome X.";
Biochim. Biophys. Acta 1492:522-525(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z39Ig
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         'Generation
                                                                                                                                                                    EQUENCE
                                                                                                                                                                                           neration and initial analysis of more than 15,000 full-length human mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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eingold E.A., Grouse L.H., Derge J.G.,
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12, Last sequence update)
28, Last annotation update)
(V-set and immunoglobulin domain containing
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Q8VBZ9
Q8VBZ9
Q72PX7
Q7T0V5
Q8N2P7
Q8QFP9
Q8UVU1
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       Potential.
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Best Local
bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AY358341; AAQ88707.1; -.
InterPro; IPR003199; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 1.
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                                                                                                                                                                                                                                                                                                                                    MEDINE-22887296; PubMed-12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Dewd P. Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   RP SEQUENCE FROM N.A.

RP STRAIN=FVB/N; TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Allausner R.D., Gollins F.S., Wang J., Hsieh F.,

RA Alleschuk R.F., J., Wang J., Hong L., Schetz T.E.,

RA Hopkins R.F., J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mahiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Alnes S. J., Marra M.A.;

RA Alnes S. J. Arra M.A.;
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Mammalia; Eutheria; Rodentia;
MCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGV;
PROSITE; PS50835; IG
SEQUENCE 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
           SEQUENCE FROM STRAIN=FVB/N;
                                                                                                                                            Jones S.J., Marra M.A.; "Generation and initial analysis
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FROM N.A.
VB/N; TISSUE=Liver;
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BC025105.
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Pred. No. 7.5e-1
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                                                                                            99:16899-16903 (2002)
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Best Local (
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                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99323940; PubMed=10395639;
MEDLINE-10323940; PubMed=10395639;
                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11 receptor) (UNQ264/PRO301).
Name=F11R; Synonyms-JAM1, JCAM;
                                                                                                                                                                                                                                                                                                                   JAM1_HUN
Q9Y624;
                                                                                                        "Combined treatment of TNF-alpha of junctional adhesion molecule J. Immunol. 163:553-557(1999).
                                                                                                                                         Ozaki H., Ishii K., H
Iwamatsu A., Kita T.;
                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; BC05105; AAH25105.1; -.
MGD; MGI:2679720; BC025105.
  SEQUENCE FROM N.A
                                                                   Sobocka M.B.,
                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like. PROSITE; PS50835; IG_LIKE; 1.
                                              Molecular cloning
                                    superfamily
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                        (NOV-1999)
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Sobocki T., Rushbrook J.I.,
                                    member
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                                 and sequencing ber from human p
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                        rom human platelets.";
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                                              F11 receptor,
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RA Strausberg R.D., Felingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stepleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse column and mouse column."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21154917; PubMed-11230166; DOI-10.1101/gr.154701; Mismann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bueersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane protein bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 28-42.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                        FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

SUBUNIT: Interacts with the first PDZ domain of PARD3. The
                    association
                                                                                                                                                                                                                                                                                        peptide prediction
                                                                                                                                                                                                                                        cleavage sites.";
Sci. 13:2819-2824(2004).
                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences.";
l. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                      between
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Matches 65
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EMBL; AF207907; AAF22829.1; -.
EMBL; AF172398; AAD48877.1; -.
EMBL; AX136649; CAB66584.1; -.
EMBL; AY358896; AAQ89255.1; -.
EMBL; BC001533; AAH01533.1; -.
Q10465;
Q10465;
01-NOV-1996
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DOMAIN
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GO; GO:0005911; C:intercellular
GO; GO:0006954; P:inflammatory z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A59406; S56749.
PDB; 1NBQ; X-ray; A/B=25-233.
Genew; HGNC:14685; F11R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein (Potential). TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like V-type 2.
Potential.
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Pred. No. 8.3e
%6; Mismatches
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N-linked (GlcNAc. .
; D95DE2FEA23D2851 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing; Glycoprotein;
t; Signal; Tight junction; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Junctional adhesion molecule
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                                                                                                                                                                   NGEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH
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Q8WZ42;
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InterPro; IPR003598; Ig c2.
InterPro; IPR004168; PPAK motif.
Pfam; PF02818; PPAK; 53.
SMART; SM00408; IGc2; 43.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, Elastic titin (Fragment).
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STRAIN=Berkeley; TISSUE=Skeletal
MEDLINE=96026330; PubMed=7569978;
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GO:0008307; F:structural constituent of
GO:0006941; P:striated muscle contraction
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                                                                                                                                                                                                                                                                                                                                                              ---NOVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYK 179
                                                                                                                              QATLKGSLPITVTWLKD-SDE--ITEDDNIRMTFENNVASLYLSGIEVKH--
                                                                                                                                                                                                                                    YFTKEFKPIEVLKEYDVMLLAEVAGTPPFEITW-----FKDNTILRSGRKYKTFIQD
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                                                                                                                                                       ASGCSSDEPTSQNLGNNYSDEPCIGQEYQIIAQINGNYARL-LDTVPLDYEFLATEGKSV 398
                                                                                                                                                                                 HLVSLQILKFVAADAGEYQCRVTNEVGSSICSARVTLREPPSFIKKIESTSSLRGGTAAF
                                                                                                                                                                                                       LIISLCCM-VVFTMAYIMLCRKTSQQEHVYEAARAHAREAN-----DSGETMR--VAIF
                                                                                                                                                                                                                                                                                                            QQTNNQEPIK-----VATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSS
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             PRELIMINARY;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178; DB 2;
Pred. No. 0.00069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B85240533CBADE58 CRC64;
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Pfam; PF00041; fn3;
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01-MAR-2004 (
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Submitted (JUL-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21573839; PubMed=11717165;
Bang M.L., Centner T., Fornoff F., Geach F
McNabb M., Witt C.C., Labeit D., Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE=20309627; PubMed=10850961;
Freiburg A., Trombitas K., Hell W.,
Centner T., Kolmerer B., Witt C., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete gene sequence of titin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GÓ:0016020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004896; F:hematopoietin/interferon-class (D200-domain.
GO:0004674; F:protein serine/threonine kinase activity; IE.
GO:0004674; F:structural constituent of muscle; IEA.
GO:0008307; F:structural constituent of muscle; IEA.
GO:0007517; P:muscle development; IEA.
GO:0006468; P:protein amino acid phosphorylation; IEA.
                                              5181
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1TNN; NMR; @=33480-33579.
1TNN; NMR; @=33480-33579.
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to I-band linking system.";
Res. 89:1065-1072(2001).
                                                                                                                               DSSGALIVQEPPSFVTKPGSKDV-LPGSAVCLKSTFQGSTPLTIRWFKGNKELVSGGSCY
                                                                                                                                                                           DTYGRPILEVPES-VTGPWKGDVNLP----CTYDPLQGYTQVLVKW-----LVQRGSDP
                                                                                   VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG--
  ---NQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYK
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                                                                                                                                                                                                                                                                                                                5B1120058A7CE58A CRC64;
                                            KEALESSLELYLVKTSDSGTYTCKVS-NVAGGVE
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                                                                                                          A33_HUMAN
Q99795;
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                        POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=97396159; PubMed=9245713; DOI=10.1006/bbrc.1997.6966;
Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.
                                                                                                                                                                                                                                                                                                                                                                               Heath J.K., White S.J., Johnstone C.N., Catimel B., Simps Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-NOV-1997 (Rel.
05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                Simpson R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97165045;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=GPA33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell surface A33 antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                        SIMILARITY: Contains 1 immunoglobulin-like C2-type domain SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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Catimel B., Simpson R.J.,

Croenen L.C.,
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PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                  TISSUE=Larvae;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                          Name=zgc:103642;
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Genew; HGNC:4445; GPA33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U79725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005887; C:integral to GO:0004872; F:receptor act
                                                                                                                               TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602171;
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                                                                                                                                                                                                                                                                                                                                                                               KRYNILNOEQPLAQPASGQPVSLKNIST-----DTSGYYICTSSNEEGTQ
                                                                                                                                                                                                                                                                                                                                                                                                            YKOOTNNOE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPISYIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTERVVIW-PFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKV-PGDVSLQLSTLEMDDRSHYTCEVTWQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLWTLCAVRVTVDAIS----VETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGLLLLGHLTVDTYGRPILEVPESVTGPWKG-DVNLPCTYDPLQGYTQVLVKW--LVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing; bulin domain; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50835;
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(TrEMBLrel.
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235
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27.5%;
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28,
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                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                         PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSE
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9; Mismatches
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N-linked (GlcNAc...
N-linked (GlcNAc...
                                                                                                                                                          ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 177;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig-like V-type.
Ig-like C2-type.
Poly-Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
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Potential.
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                          (Danio rerio).
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Palmitate; Signal;
                                                                                                                                                                                                                                                                                                     292
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les 94;
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Q8WMV3
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                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                        SEQUENCE FROM N.A.

MEDLINE=21547769; Pubmed=11688979; DOI=10.1006/bbrc.2001.5851;

MEDLINE=21547769; Pubmed=11688979; DOI=10.1006/bbrc.2001.5851;
                    Biochem.
                                                Thoelen I., Keyaerts E., Lin "Characterization of a cDNA"
                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                             Bovinae;
                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                            Coxsackie virus and
                                                                                                                                                                                                                                                                      Q8WMV3
                              adenovirus receptor.";
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    em. Biophys.
AY033651; A
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                                                                                                                                               Bos.
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PRELIMINARY;

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Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

adenovirus

, Last sequence up , Last annotation irus receptor BCAR

on update)

BCAR

20,

Created)

AAK57804.1; Res. Commun.

encoding

bovine

288:805-808 (2001)

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PROSITE;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00408; IGC2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Director MGC Project;
Submitted (SEP-2004) to the
EMBL; BC081502; AAH81502.1;
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50835; IG LIKE; 2.
292 AA; 32091 MW;
                                                                                                                                                                                                                                                                                                           MNVFNGNLEFPSVSKMDTGSYFCEASNGEGVPQRGDEVKMEVRD
                                                                                                  VPPAKPVSRIPSSVTTSSNVRLTCFDPVGSPPSTYKWYKDNTPLPEDPTKFPAFKNLTYK
                                                                                                                                                KPTVTTGSGYGFTVPQGMRISLQC-QARGSPPISYIWYKQQTN-NQBPIKVATLSTLLFK
                                                                                                                                                                                                                                                YQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVS
                                                                                                                                                                                                                                                                                                                                                           SVTGPWK----GDVNLPCTYDPLQGYTQVLVKWLVQ--RGSDPVTIFLRDSSGDHIQQAK
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                -PAVI-ADSGSYFCTAKGQVGSEQHSDIVKFVVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%;
                                                                                                                                                                                                     -DKGLRFNKVTRADTGDYDCEVSGSGGYGENTI
                                                                                                                                                                                                                                                                                                                                                                                                           25;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 170.5; 1
Pred. No. 3.5e
Pred. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99:16899-16903 (2002).
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1es 94;
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  223
                                                232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                292;
                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                           DGKPTGQ
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                         JAM1 BOVIN
Q9XT56;
16-OCT-2001
16-OCT-2001
MEDLINE-99323940; PubMed-10395639;
Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto
Iwamatsu A., Kita T.;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Junctional adhesion molecule 1 precursor (JAN
Name=F11R; Synonyms=JAM1;
                                                                                                                                                                                                                                                                                                                                                                                                          BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P78310; 1KAC.
GO; GO:0004872; F:receptor activity;
SMART; SM00408; IGC2; 1.
PROSITE; P850835; IG_LIKE; 2.
                                                                                                                                                                 "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";
J. Immunol. 163:553-557(1999).
                                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JC7780; JC7780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVGSDQ------CLLRLDVVPPSNR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFKLKCEPKEGSLPLRYEWQKLSDSQKLPTSWLPEMTSPVISVKNASAEYSGTYTCTVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RISLQCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVKWLVQRGS----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQ----GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGJ----AVIGTLLALVLIALIVP-----CCHKKRREEKYEKEVHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLSDIGTYQCKVKKAPGVGNK------KIQLTVLVKP-----SGIRCYVDGSEEIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MELLLRFLLLCGVADFTRGLSI-TTPEQMIEXAKGETAYLPCKFTLGPEDQGPLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -IEWLLSPADNOKVDQVIILY---SGDKIYDDYYODLKGRVHFTSNDLKSGDASINVTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AA; 40153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 170;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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RESULT 11
Q8VC39
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Matches 63
                                                                                QBVC39 PRELIMINARY; PRT; 300 AA. QBVC39; QBVC39; QTEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Flir protein (Mus musculus adult male cecum cDNA, R1 enriched library, clone:9130004624 product:junction molecule, full insert sequence).
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DISULFID
DISULFID
CARBOHYD
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DOMAIN
DOMAIN
                                  Eukaryota;
Mammalia; !
SEQUENCE
                  NCBI_TaxID=10090;
                                                          Mus musculus (Mouse)
                                                                         Name=F11r;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 1g; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains
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FROM N.A
                                                                                                                                                                                                                                   GYASPVKSDTV
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                                 ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR007110; Ig-like.
IPR003598; Ig_c2.
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N-linked (GlcNAc...)
714FE1C1714769A2
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Pred. No. 4.3e-05;
1; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like V-type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Junctional adhesion molecule Extracellular (Potential).
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                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                           -QOTNIQEPIKVATLSTLLFKPAVIADSGSYFCTAKG
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                                                                                                            RIKEN full-length
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; Murinae; Mus
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RX MEDLINE=2238855; pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RK Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Hopkins R.F., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hilashesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Kozywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
MEDDINE=20530913; pubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer."; [8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Cecum;

MEDLINE=20499374; pubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [7]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Cecum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum;
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STRAIN=C57BL/6J; TISSUE=Cecum;
MEDLINE=21085660; PubMed=11217851;
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STRAIR=C57BL/6J; TISSUB=Cecum;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carminci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length
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420:563-573(2002).
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on functional annot
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OK Sus 8
OC Eukar
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Best Local S
Matches 75
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                                                                                                                                                                                                                                                                          Q9TU79 PRELIMINARY; PRT; 319 AA.
Q9TU79;
Q1TU79;
Q1TU79;
Q1TU79;
Q1TU79;
Q1TU79;
Q1TU79;
Q1TEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Coxsackie-adenovirus-receptor homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO;
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                          TISSUE=Liver
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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STRAIN=C57BL/6J; TISSUE=Cecum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005615; C:extracellular space; T
GO:0016021; C:integral to membrane;
GO:0005515; F:protein binding; IPI.
m; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:1321398; F11r.
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300 AA; 32423 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GONYGEVSIHLTV-LVPPSKPTISVPS----SVTIGNRAVLTCSEHDGSPPSEYSWFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTALVCYNSQI-----TAPYADRVTFSSS-----GITFSSVTRKDNGEYTCMV---SEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV 279
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Haack A.,
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                                PubMed=10490761;
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                                                                                                                                                                   Chordata; Cranial Cetartiodactyla;
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  Wang
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Pred. No. 5.6e-
38; Mismatches
                                                                                                                                                                   Craniata; Vertebrata;
actyla; Suina; Suidae;
  Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LLFKPAVIADSGSYFCTAKGQVGSEQH
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     Eizema
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.6e-05;
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     Pauschinger
                                                                                                                                                                         Euteleostomi;
Sus.
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aka T.,
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Q9TU80
ID Q9TU8
AC Q9TU8
AC Q9TU8
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DT 01-MA
DT 01-OC
DE COXES
OC EURAS
OC EURAS
OC MAMMA
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RR P SEQUE
RA SCHOC
RT "EXPINATION CO
RT VECTO
RT GENE
DR HSSEL
DR GO; CC
DR Inter
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Best Local S
Matches 83
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Q9TU80;
01-MAY-2000
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NON TER
SEQUENCE
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-breed German shepherd; TISSUE-Liver;
MEDLINE-99422053; PubMed-10490761;
Pechner H., Haack A., Wang H., Wang X., Eizema K.,
Schoemaker R.G., van Veghel R., Houtsmuller A.B.,
Lamers J.M.J., Poller W.;
"Expression of Coxsackie-adenovirus-receptor and a
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Coxsackie-adenovirus-receptor homolog (Fragment).
Canis familfaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Verrebrata,
Eukaryota, Metazoa, Chordata, Craniata, Canidae,
  EMBL; AP109645; AAF01256.1;
HSSP; P78310; 1EAJ.
GO; GO:0004872; F:receptor :
InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00408;
PROSITE; PS5083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF109646; AAF01257.1;
HSSP; P78310; 1KAC.
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Gene Ther. 6:1520-1535(1999).
                                                                                                                        vector barriers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not correlate with adenovector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schoemaker R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; GO:0004872; P:receptor activity;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig-c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoemaker R.G., van Veghel R., Houtsmuller A.B.,
Lamers J.M.J., Poller W.;
"Expression of Coxsackie-adenovirus-receptor and
                                                                                                                                                       correlate with adenovector
                                                                                                   Ther. 6:1520-1535(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QL9DIGTYQCKVKKAPGVGNK------KIQLTVLLKPSGTRCYVDG-SEEIGNDFKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IEWLLSPADNQKVDQVIILY---SGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCEPKEGSLPLLYEWQKLSNSQKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGS
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319 /
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F:receptor ac
7110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGC2; 1.
5; IG_LIKE; 2.
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35301 MW;
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16-OCT-2001 (Rel. 4

16-OCT-2001 (Rel. 4

25-OCT-2004 (Rel. 4
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Winkler F.K.,
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Receptor.
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SEQUENCE
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J. Cell F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
Junctional adhesion molecule 1 precursor (J
Name=Filr; Synonyms=Jam1, Jcam, Jcam1;
                                                                                                                                                                       MEDIINE=21340266; PubMed=11447115; DOI=10.1093/emboj/20.14.3738; Ebnet K., Suzuki A., Horikoshi Y., Hirose T., Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.; "The cell polarity protein ASIP/PAR-3 directly associates with junctional adhesion molecule (JAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=98327120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
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SMART; SM00408; IGc2; 1.
                                                                          MEDLINE=21391702;
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  391702; PubMed=11500366; DOI=10.1093/emboj/20.16.4391;
. Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
Mueller F., Bazzoni G., Dejana E., Bartfai T.,
K., Hennig M.;
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chneemann M., Williams L.,
ciaro A., Ruco L., Villa A.
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                                                                                                                                                                                                                                                                                                                                                             3D-structure; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epithelial and endothelial cells.
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Involved in platelet activation.
SUBUNIT: Interacts with the first PDZ domain association between PARD3 and PARD6B probably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Localized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein (Potential). Localized at tight junctions of both epithelial and endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      association between interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1F97; X-ray; A=27-238.
MGI:1321398; F11r.
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Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like V-type 2.
Potential.
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  TISSUE=Prostate;
MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler R. L., Collins F.S., Wagner L., Shenmen C.M., Schuler R. L., Caberg B., Buetow K.H., Schaefer C.F., Bhat N. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F. L., Wang J., Hong L.,
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Choro
Mammalia; Eutheria; Rodes
 Diatchenko L.,
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8; Mismatches 127
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratene P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Moriguez A.C., Grimwood J. W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local S
Matches 64
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 2.
SMART; SM00406; IGv; 1.
SMO0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 300 AA; 32369 MW; 4
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Submilted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF276998; AAF78250.1; -.
EMBL; BC065309; AAH65309.1; -.
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2: /cgn2 6/ptcdata/2/pubpaa/US06 NEW PUB.pep:*

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130, Appl 130, A
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US-09-833-245-1236
US-09-833-245-1236
Sequence 1236, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/29, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-04-25
VUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1236
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.4e-179;
); Mismatches 0;
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APPLICANT: HUMAN Genome Sciences, Inc.
APPLICANT: HUMAN Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/226, 931
PRIOR APPLICATION NUMBER: 60/196, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1237
LENGTH: 399
TYPE: DEFM
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ORGANISM: Homo sapiens
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; Publication No. US20040009950A1
; GENERAL INFORMATION: BABLO D.
; APPLICANT: GARCIA, Pablo D.
; TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/10/458,143
; CURRENT FILING DATE: 2003-06-09
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: US/PRIOR FILING DATE: 2000-04-10
; PRIOR PRIOR APPLICATION NUMBER: PRIOR APPLICATION: US/SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 399
; TYPE: PRT
GORGANISM: Homo sapiens
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Best Local Similarity 100.0%;
Matches 399; Conservative 0
                                                                                                                           APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/310,025
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Pred. No. 2.4e-179;
0; Mismatches 0;
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360

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Gaps

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; PRIOR FILING DATE: 2001-08-03; PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2001-11-29; NUMBER OF SEQ ID NOS: 230; SOFTWARE: PATENTIN VEY: 2.1; SEQ ID NO 225; LENGTH: 399
APPLICANT: Gurney, Nautin I.
APPLICANT: Mapter, Mary A.
APPLICANT: Tymas, Daniel
APPLICANT: Tymas, Daniel
APPLICANT: Van Lookren, Menno
APPLICANT: Wood, William I.
TITLE OF INVENTION: USE OF A33 ANTIGENS AND JAN
FILE REFERENCE: 39766/0100P1
CURRENT PILING DATE: 2003-07-31
CURRENT FILING DATE: 2003-07-31
PRIOR PILING DATE: 2002-10-03
PRIOR PILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/12678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PILING DATE: 2000-13-01
PRIOR APPLICATION NUMBER: PCT/US0/32678
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US-10-633-008-32
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Best Local Similarity
Matches 399; Conserv
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ORGANISM: Homo sapiens
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Goddard, Audrey
Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
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; LENGTH: 399
; TYPE: PRT
; ORGANISM: homo s
US-10-656-269-42
                                                                                                                                                                                                                                          APPLICANT: Bachmann, Martin
APPLICANT: Vogt, Lorenz
ITILE OF INVENTION: Immune Modulatory Compounds and FILE REFERENCE: 1700.0390002
CURRENT APPLICATION NUMBER: US/10/656,269
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/408,233
PRIOR APPLICATION NUMBER: 60/408,233
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/449,583
PRIOR FILING DATE: 2003-02-26
NUMBER: 06/449,583
PRIOR FILING DATE: 2003-02-26
NUMBER: 07 SEQ ID NOS: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/10656269 Publication No. US20040152105A1 GENERAL INFORMATION:
                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.2 SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
SEQ ID NO 32
LENGTH: 399
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                                                                    Query Match 100.0%; Score 2098; DB 16; Best Local Similarity 100.0%; Pred. No. 2.4e-179; Matches 399; Conservative 0; Mismatches 0;
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
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                      MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
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GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

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RESULT 7
US-09-978-295A-52
                                          TITLE OF INVENTION: Secreted and Transmembrane TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06249
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
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            OR APPLICATION NUMBER: 09/918585
OR FILING DATE: 2001-07-30
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OR APPLICATION NUMBER: 60/064249
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/065311
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/077450
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Botstein, David
Desnoyers, Luc
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Gao, Wei-Qiang
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Williams, P. Mickey
Wood, William I.
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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lton, David L.
wart, Timothy A.
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-01
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APPLICATION 1
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OR FILING DATE: 1998-03-11
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OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078886
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OR APPLICATION NUMBER: 60/078936
OR APPLICATION NUMBER: 60/078910
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OR FILING DATE: 1998-03-20
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OR APPLICATION NUMBER: 60/078939
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OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/079294 OR FILING DATE: 1998-03-27

OR APPLICATION NUMBER: 60/079689

OR FILING DATE: 1998-03-27

OR APPLICATION NUMBER: 60/079663

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OR APPLICATION NUMBER: 60/079728

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OR FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 APPLICATION NUMBER: 60/079923 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/080105 APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920 APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077641
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079656 60/081817 60/081203 60/081195 60/081071 60/081049 60/081070 60/080328 60/080327 60/080165 60/080107

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569

FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22

PRIOR

OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083392
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OR APPLICATION NUMBER: 60/083495
OR APPLICATION NUMBER: 60/083495

APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797

FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796

APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29

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APPLICANT: KIO, SOPHIA S.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263091C27
CURRENT APPLICATION NUMBER: US/09/978,697
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US-09-978-697-52
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OR FILING DATE: 1998-05-15
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OR FILING DATE: 1998-05-15
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Gao, Wei-Qiang
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Filvaroff,
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Kuo, Sophia S.
                                                                                                                                                                                                                       Hillan, Kenneth
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OR APPLICATION NUMBER: 60/08358
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/08359
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OR APPLICATION NUMBER: 60/084411
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PRIOR APPLICATION NUMBER: 60/081203 PRIOR PILING DATE: 1998-04-09 PRIOR PILING DATE: 1998-04-09 PRIOR PILING DATE: 1998-04-09 PRIOR PILING DATE: 1998-04-15 PRIOR PILING DATE: 1998-04-21 PRIOR PILING DATE: 1998-04-22 PRIOR PILING DATE: 1998-04-23 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-05-07			
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR HILING DATE: 2001-07-30
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PRIOR PRILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077649
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OR APPLICATION NUMBER: 60/085700
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OR APPLICATION NUMBER: 60/085689
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Similarity 100.0%; Pred. No. 1e-142;
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Godowski, Paul J.
Grinaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Desnoyers, Luc
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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FILLE REFERENCE: P2630PIC9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR PRIOR DATE: 1997-11-03

PRIOR PRICING DATE: 1997-11-03

PRIOR PRICING DATE: 1997-11-03

PRIOR PRICING DATE: 1997-11-13

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PRIOR PRICING DATE: 1997-11-21

PRIOR PRICING DATE: 1999-31

PRIOR PRICING DATE: 1999-31

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PRIOR PRICING DATE: 1998-33-11

PRIOR APPLICATION NUMBER: 60/077641

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PRIOR PRICING DATE: 1998-33-11

PRIOR PRICING DATE: 1998-33-12

PRIOR PRICING DATE: 1998-33-13

PRIOR PRICING DATE: 1998-33-13

PRIOR APPLICATION NUMBER: 60/078004

PRIOR PRICING DATE: 1998-33-13

PRIOR APPLICATION NUMBER: 60/078806

PRIOR PRICING DATE: 1998-33-13

PRIOR APPLICATION NUMBER: 60/078806

PRIOR PRICING DATE: 1998-33-13

PRIOR APPLICATION NUMBER: 60/078806
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/07963
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079786
OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/07/632
OR APPLICATION NUMBER: 60/07/641
OR PILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/07/649
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/07/791
OR APPLICATION NUMBER: 60/07/791
OR APPLICATION NUMBER: 60/07/91
OR APPLICATION NUMBER: 60/07/8004
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/07/8866
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/07/8936
OR APPLICATION NUMBER: 60/07/8936
OR APPLICATION NUMBER: 60/07/8936
OR APPLICATION NUMBER: 60/07/8939
                     OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/08
OR APPLICATION NUMBER: 60/08
OR APPLICATION NUMBER: 60/08
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923
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Wood, William
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Shelton, David L.
Stewart, Timothy A.
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                                                           NUMBER: 60/080327
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PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/08033
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-03
PRIOR PILING DATE: 1999-04-08
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OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
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OR APPLICATION NUMBER: 60/085573
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R FILLING DATE: 1998-05-07
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OR APPLICATION NUMBER: 60/08
OR FILLING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/08
OR FILLING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08
OR FILLING DATE: 1998-05-03
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R FILING DATE: 1998-05
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                                                                                                                                             TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
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                                                                                                           TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
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Pred. No. 1e-142;
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Sequence 2, Application US/09953499
Publication No. US20020182206A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.

RESULT 10 US-09-953-499-2

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APPLICANT: NADIER, MATY A.
APPLICANT: TUMAS, DANIE!
APPLICANT: WOOD, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFERENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465
PRIOR APPLICATION NUMBER: US/09/254,465
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 30
PEQ ID NO 2
PRIOR SEQ ID NOS: 30
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Matches 321
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APPLICANT:
APPLICANT:
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TYPE: PRT |
ORGANISM: Homo sapiens
-09-953-499-2
                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
                                                                     Fong, Successions Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                            TEAPTIMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
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                                                                                                                                                                                                                         Ashkenazi, Avi
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                    Botstein, David
Desnoyers, Luc
                                                 Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                    Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                        Eaton, Dan
                                                                                                                                                                                                       Baker Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 80.5%; Score 1688; DB 9; ilarity 100.0%; Pred. No. 1e-142; Conservative 0; Mismatches C
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR TILING DATE: 2001-07-30
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-03
PRIOR PELLING DATE: 1997-11-03
PRIOR PELLING DATE: 1997-11-03
PRIOR PELLING DATE: 1997-11-33
PRIOR PELLING DATE: 1997-11-33
PRIOR PELLING DATE: 1997-11-34
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PRIOR PELLING DATE: 1998-03-10
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PRIOR PELLING DATE: 1998-03-10
PRIOR PELLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07763
PRIOR PELLING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/07764
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PRIOR PELLING DATE: 1998-03-13
PRIOR PELLING DATE: 1998-03-13
PRIOR PELLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078886
PRIOR PELLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PELLING DATE: 1998-03-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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OR APPLICATION NUMBER: 60/079786
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923
OR APPLICATION NUMBER: 60/079923
OR APPLICATION NUMBER: 60/080105
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080107
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080165
DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079663
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuo, Sophia S.
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DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080327

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080328

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080333

DR FILING DATE: 1998-04-01

DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080333

APPLICATION NUMBER: 60/081071 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081195

FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
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Best Local Sim
Matches 321;
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OR FILING DATE: 1998-05-06
OR APPLICATION NUMBER: 60/084639
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084639
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084640
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084598
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OR APPLICATION NUMBER: 60/08532
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08532
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085582
OR APPLICATION NUMBER: 60/085583
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085583
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 301
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                         MAYIMLCRKTSQQEHVYEAAR
                                                                                                TEAPTIMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
                                                                                                                                                QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVXDSSKLLKTK
                                                                                                                                                                        QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
                                                                                                                                                                                                                        DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ
                                                                                                                                                                                                                                           DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ
MAYIMLCRKTSQQEHVYEAAR
                                                                                                                                                                                                                                                                                                 GSDPVT1FLRDSSGDH1QQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
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Pred. No. 1e-142;
0; Mismatches 0;
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PRIOR

DR FILING DATE: 1998-04-08

TRAPLICATION NUMBER: 60/081203

TRAPLICATION NUMBER: 60/081229

PRILING DATE: 1998-04-09

PRILING DATE: 1998-04-15

PRILING DATE: 1998-04-21

PRILING DATE: 1998-04-22

PRILING DATE: 1998-04-23

PREPLICATION NUMBER: 60/082796

PRILING DATE: 1998-04-29

PRAPPLICATION NUMBER: 60/08332

PRILING DATE: 1998-04-29

PRAPPLICATION NUMBER: 60/083496

PRILING DATE: 1998-04-29

PRAPPLICATION NUMBER: 60/083496

PREPLICATION NUMBER: 60/083559

PREPLICATION

RESULT 12
US-09-978-189-52
; Sequence 52, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PELICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077632
PRIOR PILING DATE: 1998-03-11
PRIOR PRIOR PILING DATE: 1998-03-11
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James,
APPLICANT: Pan, James,
APPLICANT: Pani, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
TITLE OF INVENTION ACIDS Encoding the Same
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                                                                                                                    PRIOR
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CURRENT FILING DATE: 2001-10-15
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DR FILING DATE: 1998-03-11

PR APPLICATION NUMBER: 60/077649

PR FILING DATE: 1998-03-11

PR APPLICATION NUMBER: 60/077791

PR APPLICATION NUMBER: 60/077910

PR FILING DATE: 1998-03-12

PR APPLICATION NUMBER: 60/078004

PR FILING DATE: 1998-03-20

PR APPLICATION NUMBER: 60/078936

PR FILING DATE: 1998-03-20

PR APPLICATION NUMBER: 60/078936

PR FILING DATE: 1998-03-20

PR APPLICATION NUMBER: 60/078939

PR APPLICATION NUMBER: 60/078939

PR FILING DATE: 1998-03-20

PR APPLICATION NUMBER: 60/079294

PR FILING DATE: 1998-03-25

PR APPLICATION NUMBER: 60/079294

PR APPLICATION NUMBER: 60/079294

PR APPLICATION NUMBER: 60/079666

PR APPLICATION NUMBER: 60/079666

PR APPLICATION NUMBER: 60/079669

PR APPLICATION NUMBER: 60/079669

PR APPLICATION NUMBER: 60/079663

PR APPLICATION NUMBER: 60/079728

PR APPLICATION NUMBER: 60/079728
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
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Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filvaroff,
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f, Ellen
     PATION PA
OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR APPLICATION NUMBER: 60/083332
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083392
OR APPLICATION NUMBER: 60/083495
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083499
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OR APPLICATION NUMBER: 60/083499
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083545
OR APPLICATION NUMBER: 60/083545
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OR APPLICATION NUMBER: 60/082569
OR APPLICATION NUMBER: 60/082569
OR APPLICATION NUMBER: 60/082704
OR APPLICATION NUMBER: 60/082804
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082700
OR APPLICATION NUMBER: 60/082797
OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR APPLICATION NUMBER: 60/082797
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DR APPLICATION NUMBER: 60/080334

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/081070

DR FILING DATE: 1998-04-08

DR APPLICATION NUMBER: 60/081049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/
FILING DATE: 1998-03-31
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/080107
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RR FILLING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/08582

RR FILLING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/085700

DR FILING DATE: 1998-05-15
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R FILLING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085338
R FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085704
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APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60/084640
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FILING DATE: 1998-05-06
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER:
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APPLICANT: Ashkenazi, Avi
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Publication No.
                                                                                                                                                                                                                                                                           Matches 321;
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CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillar Venneth J.
                                                QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
                                                                                                            DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ
TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
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                                                                                           DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ
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Botstein, David
Desnoyers, Luc
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Williams, P. Mickey
Wood, William I.
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Vo. US20030045462A1
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Stewart, Timothy A.
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Kljavin, Ivar J.
Kuo, Sophia S.
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Gao, Wei-Qiang
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Ef, Ellen
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Pred. No. 1e-142;
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SEQ ID NO 52
LENGTH: 321
TYPE: PRT
ORGANISM: Homo Bapiens
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: P263091C15
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               QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
                                    QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                                                      DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ
                                                                                                                                                           GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
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Gerritsen, Mary E.
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Desnoyers, Luc
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Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                                         80.5%; Score 1688; DB 10; Length 321; llarity 100.0%; Pred. No. 1e-142; Conservative 0; Mismatches 0; Indels 0
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
             PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1997-11-03
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FILING DATE: 1998-03-12
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Godowski, Paul J.
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Gao, Wei-Qiang
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Kuo, Sophia S.
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f, Ellen
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PCT-US00-31162A-63

Sequence 63, Application PC/TUS0031162A

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: 18 Human Secreted Proteins

FILE REFERENCE: PS717PCT

CURRENT APPLICATION NUMBER: PCT/US00/31162A

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: 60/166,415

PRIOR APPLICATION NUMBER: 60/215,136

PRIOR APPLICATION NUMBER: 60/215,136

PRIOR PILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PATENTIN OF SEQ ID NOS: 161

SOFTWARE: PATENTIN VET. 2.0

JEQ ID NO 63

LENGTH: 399

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US00-31162A-63
 Query Match
Best Local Sim
Matches 399;
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                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative
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Score 2098; DB 1;
Pred. No. 2.6e-193;
); Mismatches 0;
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S-10-125-921A-388
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; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local S
Matches 399
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 18 Human Secreted
FILE REFERENCE: PS717PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US00/31162A CURRENT FILING DATE: 2000-11-15 PRIOR APPLICATION NUMBER: 60/166,415 PRIOR FILING DATE: 1999-11-19 PRIOR APPLICATION NUMBER: 60/215,136 PRIOR APPLICATION NUMBER: 60/215,136 PRIOR FILING DATE: 2000-06-30
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                                                                                                                        DGNQVVRDKITELRVQKLSVSKÞTVTTGSGYGFTVÞQGMRISLQCQARGSÞÞISYIWYKQ
                                                               QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Pred. No. 2.6e-193;
; Mismatches 0;
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APPLICANT: HUMAN Genome Sciences, Inc.
APPLICANT: HUMAN Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILLING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILLING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILLING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 100.0%;
Matches 399; Conservative (
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                                                                        MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE
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                    PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC
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Pred. No. 2.6e-193;
); Mismatches 0;
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RESULT 4
PCT-US01-11988-1237
; Sequence 1237, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins

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APPLICANT: MUXTRY, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200PC
CURRENT APPLICATION NUMBER: PCT/VS02/04915
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 09/285,475
PRIOR APPLICATION NUMBER: US 60/285,475
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/310,025
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CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 1237
LENGTH: 399
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PCT-US02-04915-225
Sequence 225, Application PC/TUS0204915
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
PCT-US01-11988-1237
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Best Local Similarity
Matches 399; Conserv
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APPLICATION NUMBER: US 60/310,025
FILING DATE: 2001-08-03
APPLICATION NUMBER: US 60/350,666
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 225
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
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                     PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC
                                                                                 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE
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PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC
                                                            MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE
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Pred. No. 2.6e-193;
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Sequence 1434, Application PC/TUS0208123;
Sequence 1434, Application PC/TUS0208123;
GENERAL INFORMATION: Human Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins;
FILE REFERENCE: PS944PCT;
CURRENT FILING DATE: 2002-03-19;
PRIOR APPLICATION NUMBER: US 60/331,287;
PRIOR FILING DATE: 2001-11-13;
PRIOR APPLICATION NUMBER: US 60/306,171;
PRIOR PILING DATE: 2001-07-19;
PRIOR PRIOR APPLICATION NUMBER: US 60/277,340;
PRIOR FILING DATE: 2001-03-21;
NUMBER OF SEQ ID NOS: 2048;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 1434;
LENGTH: 399;
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08123-1434

Query Match
Best Local Similarity 100.0%; Score 2098; DB 1;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0;
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MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR

Length 399;

Indels

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PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR PILING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 857
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 592
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08124-592
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PCT-US02-08124-592
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Best Local S
Matches 399
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CURRENT FILING DATE: 2002-03-19
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS901PCT
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TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
                      TEAPTIMIYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
                                                                                            QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
                                                                                                                        QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK
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                                                                                                                                                                                                                                                                                        GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
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       RESULT 9
PCT-US02-08277-931
; Sequence 931, Application PC/TUS0208277
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Professional Professional Professional Profession
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PCT-US02-08276-446
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PCT-US02-08276-446; Apply Sequence 446, Apply Sequence 44
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FILE REFERENCE: PS907PCT
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GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.
FIITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS906PCT

CURRENT APPLICATION NUMBER: PCT/US02/08276

CURRENT FILING DATE: 2002-03-19

PRIOR APPLICATION NUMBER: US 60/331,287

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/306,171

PRIOR APPLICATION NUMBER: US 60/277,340

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 650

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 446

LENGTH: 399

TYDE: DET
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Local Similarity 100.0%;
nes 399; Conservative (
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Pred. No. 2.6e-193;
); Mismatches 0;
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Secreted Proteins

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Sequence 1373, Application PC/TUS0208278
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS902PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08278
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 1988
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 1373
; LENGTH: 399
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/207,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1357
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SEQ ID NO 931
LENGTH: 399
TYPER: DET
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PCT-US02-08278-1373
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Best Local &
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Query Match
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ORGANISM: Homo sapiens
                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.
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2.6e-193;
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Sequence 795, Application PC/TUS0209785
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; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS905PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09785
; CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 795
; LENGTH: 399
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PCT-US02-09785-795
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Similarity 100.0%;
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Pred. No. 2.6e-193;
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PCT-US03-31207-32
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Best Local Similarity
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CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 10/633,008
PRIOR FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 10/265,542
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, William I.
TITLE OF INVENTION: Use of A33 Antigens and
FILE REFERENCE: 39766-0100PCT
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ORGANISM: Homo
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Goddard, Audrey,
Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
Van Lookren, Menno
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 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
                                     MAY IMLCRKTSQQEHVYEAARAHAREANDSGETMRVAI FASGCSSDEPTSQNLGNNYSDE
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Pred. No. 2.6e-193;
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PCT US04-34163-319

PCT US04-34163-319

Sequence 319, Application PC/TUS0434163

GENERAL INFORMATION:

APPLICANT: Bayer Pharamceuticals Corporation

APPLICANT: Pauloski, Nicole

APPLICANT: Taylor, Ian

APPLICANT: Baywood, Douglas

TITLE OF INVENTION: GENE EXPRESSION PROFILES ANI

FILE REFERENCE: 5176

CURRENT APPLICATION NUMBER: PCT/US04/34163

CURRENT FILING DATE: 2004-10-01

PRIOR APPLICATION NUMBER: US 60/508,355

PRIOR FILING DATE: 2003-10-03

NUMBER OF SEQ ID NOS: 400

SCHEMBER OF SEQ ID NOS: 400
             ; Sequence 8, Application US/09546309
; GENERAL INFORMATION:
APPLICANT: GARCIA, PABLO D.
TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/09/546,309
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 30
; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; EDG ID NO 8
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US-09-546-309-8
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LENCTH: 399
TYPE: PRT
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TYPE: PRT
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Local Similarity 100.0%;
nes 399; Conservative (
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Pred. No. 2.6e-193;
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CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT PILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR PILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR PILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOPTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1236:
; LENGTH: 399
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Best Local S
Matches 399
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
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Best Local Similarity
Matches 399; Conserv
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ORGANISM: Homo sapiens
-09-833-245-1236
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Local Similarity 100.0%; Pred. No. 2.6e-193;
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Maximum DB seg length: 2000000000
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Sequence 98, Appl Sequence 301, Appl Sequence 34918, A Sequence 58505, A Sequence 1947, Ap Sequence 523, Appl Sequence 1294, Appl Sequence 1294, Appl	யமக்க	Sequence 1845, Ap Sequence 4, Appli Sequence 1805, Ap	Sequence 427, App Sequence 637, App	Sequence 27, Appl Sequence 27, Appl Sequence 328, App	Sequence 1667, Ap Sequence 1679, Ap	Sequence 987, App Sequence 1622, Ap	Sequence 115, App Sequence 555, App	Sequence 35, Appl Sequence 555, App	Sequence 33, Appl Sequence 34, Appl	Sequence 31, Appl Sequence 32, Appl	Sequence 556, App Sequence 556, App	Sequence 44206, A Sequence 105, App	Sequence 557, App Sequence 37007, A	Sequence 1703, Ap Sequence 30579, A Sequence 557, App	Sequence 584, App Sequence 635, App	Sequence 46425, A Sequence 36, Appl	Sequence 18, Appl Sequence 51718, A	Sequence 1202, Ap Sequence 52991, A	Sequence 511, App Sequence 1201, Ap	Sequence 46424, A Sequence 508, App	Sequence 1971, Ap Sequence 1986, Ap	Sequence 5, Appli Sequence 1648, Ap	Sequence 2, Appli Sequence 216, App	sequence 103, App Sequence 2060, Ap	Sequence 100, App	Sequence 440, App Sequence 58. Appl	Sequence 143, App	Sequence 40404, A	Sequence 31, Appl	Sequence 259, App	Sequence 148, App Sequence 37976, A Sequence 29, Appl
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US-11-054-515-446 US-11-054-515-476 US-11-054-515-477 US-11-054-515-477 US-11-054-515-515 US-11-054-515-515 US-11-054-515-515 US-11-054-515-580 US-11-054-515-580 US-11-054-515-639 US-11-054-515-669 US-11-054-515-669 US-11-054-515-675 US-11-054-515-679 US-11-054-515-769 US-11-054-51	75-11-054-515-435 75-11-054-515-441 75-11-054-515-441	JS-11-054-515-415 JS-11-054-515-417 JS-11-054-515-430)S-11-054-515-383 JS-11-054-515-405 JS-11-054-515-412	/S-11-054-515-360 /S-11-054-515-363	JS-11-054-515-345 JS-11-054-515-346	JS-11-054-515-1781 JS-11-054-515-333	JS-11-054-515-1568 JS-11-054-515-1477	JS-10-287-436A-1182 JS-11-054-515-1515
equence 4. equence 5. equence 6. equence 7. equence 8. equence 8. equence 9.	equence 4.	equence 4: equence 4: equence 4:	Sequence 405, Sequence 412,	equence 3	nce 3	equence 1	equence 1	quence 1: quence 1:
46, App 46, Ap	App	App	App	App	App	1. Ap	7, Ap	2, Ap
RESULT 1 US-09-978-191C-52 Sequence 52, Applicant INFORMATI APPLICANT Back APPLICANT Back APPLICANT Bett APPLICANT Bett APPLICANT Bett APPLICANT Bett APPLICANT Geo APPLICANT Nap APPLICANT Nap APPLICANT Pao APPLICANT Pao APPLICANT She APPLICANT She APPLICANT No APPLICANT No APPLICANT She APPLICANT No APPLICANT WIN APPLICA		99 74 00 74	1496 /4 1497 74 1498 74	94 74 95 74	92 74 93 74	0 74 1 74	89 74	86 74 87 , 74
TR 19		99 74 3.5 00 74 3.5	96	94 74 3.5 95 74 3.5	92 74 3.5 93 74 3.5	90 74 3.5 91 74 3.5	88 774 3.5	86 74 3.5 87 ,74 3.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 623
LENGTH: 321
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10986822 GENERAL INFORMATION:
                                                                                                                  SEQ ID NO 6
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Best Local (
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                                                                                                                              PRIOR APPLICATION NUMBER: 60/098,206
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
                                                                                                                                                                                                                             APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
FILE REFERENCE: PF-0577 PCT
CURRENT APPLICATION NUMBER: US/10/986,822
CURRENT FILING DATE: 2004-11-15
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: INCYTE PHARMACEUTICALS, APPLICANT: TANG, Y. Tom
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/763,902 PRIOR FILING DATE: 2002-08-22
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          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No:1871275CD1
                                            ORGANISM: Homo sapiens FEATURE:
                                                                                TYPE: PRT
                                                                                              LENGTH: 175
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Local Similarity 100.0%;
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CORLEY, Neil C.
GUEGLER, Karl J.
GORGONE, Gina A.
BAUGHN, Mariah R.
PATTERSON, Chandra
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CURRENT APPLICATION NUMBER: US/10/523,834
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/401,469
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 396
SOFTWARE: PatentIn version 3.1
SEQ ID NO 330
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapien
US-10-523-834-330
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                                                                                                                           112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163
                                                             164
                                                                                                                                                         116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
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                                                                                                                                                                                                                        GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
SNAVR 228
                               SDIVK 227
                                                                                                                                                                                                                                                       LAILLCSLALGSVTVHS-SEPEVRIPEN----NPVKLSCAY---SGFSSPRVEW----
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                                                             YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223
                                                                                           YIWXK----QQTN-----
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Salceda, Susana
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Sun, Yongming
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Pred. No. 1.5e-07;
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Pred. No. 1.2e-66;
                                                                                             -NOEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
                                                                                                                                                                                                                                                                                                                       Mismatches
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CURRENT APPLICATION NUMBER: US/60/651,509
CURRENT FILING DATE: 2005-02-10
NUMBER OF SEQ ID NOS: 1940
SOPTWARE: FAST-SEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-155-282B-11
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US-10-155-282B-11
                                                                                                                                                                                                                                                                         Sequence 101, Application US/60651509
GENERAL INFORMATION:
APPLICANT: RUBEN, Steven et al.
TITLE OF INVENTION: BREAST DISEASE TARGETS
FILE REFERENCE: CL001578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10155282B
GENERAL INFORMATION:
APPLICANT: Brookhaven Science Associates
APPLICANT: Freimuth, Paul I
TITLE OF INVENTION: Recombinant Soluble Adenovirus
FILE REFERENCE: BSA 02-14
                                                       Matches
                                                                                                                         -60-651-509-101
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Best Local
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                                                                                       Query Match
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CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/236,423
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 365
                                                                       Local
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 1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ
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                                                                   h 7.6%; Score 159; DB 8; Similarity 23.2%; Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOVGSEOHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKOSWDWTTDMDGYLGET 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRISLQCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAH
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                                                       Conservative
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23.2%; Pred. No. 7.3e-06;
ative 49; Mismatches 119;
                                                 49;
                                                   Mismatches 119; Indels 100; Gaps
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(GENERAL INFORMATION:
APPLICANT: RUBEN, Steven et al.
TITLE OF INVENTION: BREAST DISEASE TARGETS AN
FILE REFERENCE: CL001578
CURRENT APPLICATION NUMBER: US/60/651,509
CURRENT FILING DATE: 2005-02-10
NUMBER OF SEQ ID NOS: 1940
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103
LENGTH: 365
US-09-978-191C-59
IS-09-978-191C-59
Sequence 59, Application US/09978191C
GENERAL INFORMATION:
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; ORGANISM: Homo
US-60-651-509-103
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US-60-651-509-103
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Local Similarity 23.2%;
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156 SDFKIKCEPKEGSLPLQYEWQKLSDSQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVR
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                                                                                                                                                                                      GQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGET 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --IEWLISPADNQKVDQVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
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                                                      SAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAH
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-RKKRREEKYEKEVHH
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; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo s
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                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-03-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 2001-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/978,191C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/077791
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/077649
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                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-03-11
113 CEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQ-ARGSP 171
                                 54 TDNEGNOKVVI---TYSSRHVYNNLTEEOKGRVAFASNFLAGDASLQIEPLKPSDEGRYT
                                                                59
                                                                                                                           1 MGILLGLLLGHL--TVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLV
                                                                                                                                                           91;
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                                                             --QRGSDPYTIFLRDSSGDHIQQ---AKYQGRL-HVSHKVPGDVSLQLSTLEMDDRSHYT 112
                                                                                            MSLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLP-EKDTLD-----IEWLL
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Baker Kevin P.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I
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Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoni
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                                                                                                                                                           Conservative
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                                                                                                                                                                        22.2%;
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                                                                                                                                                                        7.6%; Score 158.5; DB 5
22.2%; Pred. No. 8.3e-06;
                                                                                                                                                           64;
                                                                                                                                                           Mismatches 154;
                                                                                                                                                                                         DB S;
                                                                                                                                                                                       Length 373;
                                                                                                                                                           Indels 101;
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US-10-450-763-32378
US-10-450-763-32378
; Sequence 32378, Application US/10450763
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-523-834-331
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SEQ ID NO 331
LENGTH: 351
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 331, Application US/10523834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Chenghua
APPLICANT: Sun, Yongming
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: DEX-0443
CURRENT PEPLICATION NUMBER: US/10/523,834
CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: diaDexus,
APPLICANT: Macina, I
APPLICANT: Salceda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/401,469 PRIOR FILING DATE: 2002-08-06
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                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 SRSSRSGSSSTRSTANSASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 VAIFASGCSSDEPTS-----QNLGNNYSDEPCIG-QEYQIIA-QINGN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 VFAIILIISLCCMVVFTMAYIMLCRKTSQQ-----EHVYEAARA-HAREANDSGETMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 DIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 PIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKE--S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
67; Conserv
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                                                                                                                                                                              -----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVK 227
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                                                                                                                                                                                                                          LIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNP
                                                                                                                                                                                                                                                                                                                   DTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMVSEEGGNSYGEVKVK
                                                                                                                                                                                                                                                                                                                                                             DHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDK 129
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Salceda, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 157.5; DB 6
23.0%; Pred. No. 9.4e-06;
tive 38; Mismatches 95
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PRIOR APPLICATION NUMBER: PCT/USO1/08631

PRIOR PILLING DATE: 2001-03-06

PRIOR FILLING DATE: 2001-03-30

PRIOR PILLING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PILLING DATE: 2000-08-23

NUMBER: OF SEQ ID NOS: 60736

SEQ ID NO 32378

LENGTH: 777
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PCT-US05-03880-128
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Sequence 128, Application PC/TUS0503880

GENERAL INFORMATION:
APPLICANT: INANA, GEORGE
APPLICANT: MCLAREN, MARGARET
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 39532-192229
CURRENT APPLICATION NUMBER: PCT/US05/03880
CURRENT FILING DATE: 2005-02-09
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (394)..(728)
OTHER INFORMATION: Immunoglobulin domain
OTHER INFORMATION: E-value=1.4e-36, PFam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (564)..(597)
OTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by OTHER INFORMATION: eMATRIX, accession number PD02870B, p-value=7.400e-10, OTHER INFORMATION: 18.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                       678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 --- LWASDKGTYICEAENOFGKIQSETTVTVTGLVAPLIGIS-PSVA-----NVIEGQ 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 LSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGM 159
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                                                                                                                                                                                                                                                                                                                                                L 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLTLPCTLLAGNPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGGEYTCVASNV 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLGLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL
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24.3%; Pred. No. 3.2e-05;
tive 38; Mismatches 128
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; LENGTH: 5622
; TYPE: PRT
; ORGANISM: Homo s
PCT-US05-03880-128
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US-11-049-637-2
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Donoho, Gregory
ITITLE OF INVENTION: Novel Human Hemicentin Pri
ITITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0235-USA
CURRENT APPLICATION NUMBER: US/11/049,637
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US/09/953,096
PRIOR APPLICATION NUMBER: US/09/953,096
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
                                                                                                                                                                               US-11-049-637-2
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRRESEQ for Windows
SEQ ID NO 2
LENGTH: 5518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/11049637
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mathur, Brian
                                                                                                                                                                                                TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(5518)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      753 LIGILKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL 812
753 LIGILKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL
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                                             LLGLLLL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGSEQHSDIVKF----VVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LWASDKGTYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA-----NVIEGQ 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARAHAREANDSGETMRVAIFAS--GCSSDEP
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                                                                                       Conservative
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                                                                                     7.3%; Score 153.5; DB 7; 25.2%; Pred. No. 0.00064; tive 38; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VRPRVFGDQRGLSQDKP 1086
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Pred. No. 0.00054;
                                             -GHLTVDTYGRPI-LEVPESVTGPWKGDVNL
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                                                                                                                                  Length 5518;
                                                                                          Indels
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US-10-450-763-32476
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SOFTWARE: Custom
SEQ ID NO 32476
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GENERAL INFORMATION
                                                                                                                                                                                                                                         Matches
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Best Local
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PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR ETLING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (270)..(303)
COTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by
OTHER INFORMATION: eMATRIX, accession number PD02870B, p-value=7.400e-10,
OTHER INFORMATION: 18.83
                                                                                                                                                                                                                                                                                                                         LOCATION: (60)..(434)
OTHER INFORMATION: Immunoglobulin domain
OTHER INFORMATION: E-value=1.4e-36, PFam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: DOMAIN
LOCATION: (60)..
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                                 275 ---LWASDKGTYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA-----NVIEGQ
                                                                 100 LSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGM 159
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RISLQCQ-ARGSPPISYIWYKQQTN-NQEP-IKVATLSTLLFKPAVIADSGSYFCTAKGQ 216
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                                                                                                   PCY---VQGYPEPTIKW---RRLDNMPIFSRPFSVSSISQLR-TGALFILN------
                                                                                                                                    PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQ
                                                                                                                                                                      LLGLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                        7.2%;
                                                                                                                                                                                                                                      ; Score 151; DB 6; Length 434; ; Pred. No. 4.3e-05; 38; Mismatches 123; Indels
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                                                                                                                                                                                                        -GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
                                                                                                                                                                                                                                                                                                                           identified by PFam, score of 122.9
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SEQ ID NO 52760
LENGTH: 361
TYPE: PRT
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Best Local |
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FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
                  Sequence 139, Application US/10852335A
GENERAL INFORMATION:
APPLICANT: HEIDI S. PHILLIPS
TITLE OF INVENTION: Compositions and I
TITLE OF INVENTION: Treatment of Tum
FILE REFERENCE: P5103R1-US
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (56)..(232)
OTHER INFORMATION: Immunoglobulin domain identified by PFam,
OTHER INFORMATION: E-value=9.6e-19, PFam score of 65.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(361)

OTHER INFORMATION: Xaa = X or * as defined in Table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 ----RKEIDEIAIEVTVQVKP-VTPVCRVPKAVPVGKMATLHCQGEXGPPPAHYSWYR- 184
                                                                                                                                                                                                                                                                                                                                                                                                                    181 QTNNQEPIKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPISYIWYKQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 EQTTYVFFDN------KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARND- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 LIGAVNLKSSNRTPVVQEFES-----VELSCIITDSQTSDP-----RIEWKKIQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LIGHLTVDTYGR-PILEVPESVTGPWKGDVNLPC----TYDPLQGYTQVLVKWLVQRG
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                  Compositions and Methods for the Diagnosis Treatment of Tumors of Glial Origin
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CURRENT APPLICATION NUMBER: US/10/852,335A; CURRENT FILING DATE: 2004-05-24; PRIOR APPLICATION NUMBER: US 60/548,299; PRIOR APPLICATION NUMBER: US 60/548,299; PRIOR FILING DATE: 2004-02-27; PRIOR PILING DATE: 2003-05-23; NUMBER OF SEQ ID NOS: 190

SEQ ID NO 139; SEQ ID NOS: 190

LENGTH: 3707; TYPE: PRT

ORGANISM: Homo sapiens
US-10-852-335A-139
                                                  CURRENT APPLICATION NUMBER: PCT/US05/02350
CURRENT FILING DATE: 2005-02-10
NUMBER OF SEQ ID NOS: 1155
SOFTWARE: Patentin version 3.3
SEQ ID NO 272
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US05-02350-272
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
TITLE OF INVENTION: SAME
FILE REFERENCE: 28487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ayalon-Soffer, Michal APPLICANT: Levine, Zurit
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Local Similarity 25.1%; Pred. No. 0.006;
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Nemzer, Sergey
Rosenberg, Avi
Dahary, Dvir
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Akiva, Pinchas
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FILE REFERENCE: P1216R1(US)
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: WS/09/254,465A
CURRENT FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-11-21
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: WS 60/078,936
PRIOR APPLICATION NUMBER: WS 60/078,936
PRIOR APPLICATION NUMBER: DST/US98/19437
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: DST/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 2
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-254-465A-2
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Best Local S
Matches 321
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 TEAPTIMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT
                              GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
                                                                                                              GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP
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US-08-702-525-19

US-09-450-798-2

US-08-403-253A-2

US-09-651-200-13

US-09-651-300-13

US-09-667-135-34

US-09-425-762-29

US-09-837-867A-19

US-09-810-174B-5

US-09-620-461-5

US-09-206-132-6
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Pred. No. 2.6e-167;
0; Mismatches 0;
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RESULT 3
US-09-369-247-63
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; ORGANISM: Homo
US-09-953-499-2
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TITLE OF INVENTION: OF DISEASES CHARACTERIZ
FILE REFERENCE: P1216R1(US)
FILE REFERENCE: P201-09-14
FRIOR APPLICATION NUMBER: US 09/254,465
FRIOR APPLICATION NUMBER: PCT/US98/24855
FRIOR FILLING DATE: 1998-11-20
FRIOR APPLICATION NUMBER: US 60/066,364
FRIOR FILLING DATE: 1997-11-21
FRIOR APPLICATION NUMBER: US 60/078,936
FRIOR FILLING DATE: 1998-03-20
FRIOR FILLING DATE: 1998-03-20
FRIOR FILLING DATE: 1998-03-17
FRIOR FILLING DATE: 1998-03-17
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LENGTH: 321
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Best Local
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APPLICANT: Ashkenazi, Avi
APPLICANT: Fong, Sherman
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                                                                                                                         MAYIMLCRKTSQQEHVYEAAR 321
                                                                                                                                                           MAYIMLCRKTSQQEHVYEAAR 321
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Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
Tumas, William I.
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US-Uy-, C.
; Sequence 6, Applicant.
; Patent No. 6838241
; Patent No. 6838241
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
, PDT.TCANT: YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: SITE
; LOCATION: (306)
; OTHER INFORMATION: X
US-09-369-247-63
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CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 60/074,118
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER FILING DATE: 1998-02-09
NUMBER: 60/074,141
EARLIER FILING DATE: 1998-02-09
NUMBER: 60/074,141
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Matches
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SEQ ID NO 63
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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TITLE OF INVENTION: 44
FILE REFERENCE: PZ024P1
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llarity 76.2%;
Conservative
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Pred. No. 1.2e-152;
D; Mismatches 1;
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180

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146 240

266 360 206 300

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Gaps

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, James APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated Fro
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
ORGANISM: Human
PEATURE:
NAME/KEY: UNSURE
LOCATION: (289)...(247)
NAME/KEY: UNSURE
LOCATION: (289)...(289)
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US-09-188-930-189
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; CRGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 68382411871275CD1
US-09-763-902B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 189, Application US/09188930A Patent No. 6150502
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Best Local &
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TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
FILE REFERENCE: PP-0577 PCT
CURRENT APPLICATION NUMBER: US/09/763,902B
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: 60/098,206
PRIOR PILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 16
SOFTMARE: PERL PROGram
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al Similarity 64.7%;
174; Conservative
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GORGONE, Gina A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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; ORGANISM: Human
US-09-188-930-331
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 331
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.5%;
Best Local Similarity 26.5%;
Matches 65; Conservative 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
TITLE REFERENCE: 11000.1011c1
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          224
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          SNAVR 228
                                                 SDIVK 227
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                                                                                          YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223
                                                                                                                              YIWYK----QQTN-----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
                                                                                                                                                                         SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE
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                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178.5; DB 3; Pred. No. 7e-10; 6; Mismatches 93;
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RESULT 8
US-09-254-465A-1
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; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09254465A Patent No. 6410708
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Patent No. 6358707
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                               CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936
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TITLE OF INVENTION: Human Fil Antigen: A Cell Surface
TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR FILING DATE: 1997-07-10
                                                                                                                                                                          TITLE OF INVENTION: COMPOUNDS, COMPOUNDS, CONTITUE OF INVENTION: OF DISEASES FILE REFERENCE: P1216R1(US)
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APPLICATION NUMBER:
                    FILING DATE:
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                                                                                                                                                                                                                                  Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNAVR 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YIWYK----QQTN-----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
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                                                                                                                                                                                                                                                                                                            Fong, Sherman
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                      Genentech, Inc.
Ashkenazi, Avi J.
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                    1998-03-
PCT/US98/19437
                                                                                                                                                                                              COMPOSITIONS AND METHODS FOR THE TREATMENT S CHARACTERIZED BY A33- RELATED ANTIGENS
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.7e-10;
.93;
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APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
ITITLE OF INVENTION: Compositions Isolated from Skin Cells
ITITLE OF INVENTION: Compositions of Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/99/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 189
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
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US-09-312-283C-189
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NUMBER OF SEQ ID NOS:
SEQ ID NO 1
                                                                                                                                                                                                                            Query Match 8.5%; Score 178.5; DB Best Local Similarity 26.5%; Fred. No. 7e-10; Matches 65; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 189, Application US/09312283C Patent No. 6573095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Homo sapiens
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                            116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
                                                                           63
                                                                                                              61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LAILLCSTALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Conservative
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                                                                                                                                                                                        1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR
                                                                                                                                                       LAILLCSLALGSVTVHS-SEPEVRIPEN----NPVKLSCAY---SGFSSPRVEW----
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Sleeman, Matthew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-09-17
                                                                           - KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE - - DTGTYTCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 178.5; DB 4;
26.5%; Pred. No. 7e-10;
tive 36; Mismatches 93;
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                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                93;
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Fatrara, Napole
APPLICANT: Filvaroff, Elle
                                                                                                                                                                                                                                                     US-09-907-794A-119
                                                                                                                                                                                                                                                                         RESULT 11
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US-09-312-283C-331
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                                                                                                                                                                                                              Sequence 119, Application US/09907794A Patent No. 6635468
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Patent No.
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APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna
                         APPLICANT:
                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            175 YIWYK----QQTN-----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE
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                                                       Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Perrara, Napoleone
Filvaroff, Ellen
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     Fong, bic. Gao, Wei-Qiang
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Sleeman, Matthew
Onrust, Rene
Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                 228
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26.5%;
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; Pred. No. 7e-10;
36; Mismatches 93;
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                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-119
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LENGTH: 299
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-11-30
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                                                                                                                                                                  8.5%;
Local Similarity 26.5%;
es 65; Conservation
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/00219 FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/30999 FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US99/28214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/28564
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                         63
                                                           61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
                                                                                                                                      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
                                                                                                   LAILLCSLALGSVTVHS-SEPEVRIPEN-----
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Grimaldi, Christopher
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Stewart, Timothy A.
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                       KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV
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                                                                                                                                                                          36;
                                                                                                                                                                          Score 178.5; DB
Pred. No. 7e-10;
6; Mismatches
                                                                                                                                                                                                              DB 4;
                                                                                                   -NPVKLSCAY---SGFSSPRVEW----
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                                                                                                                                                                            Indels
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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OR FILING DATE: 1999-07-07
OR APPLICATION NUMBER: US 60/145,698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: US 60/146,222
OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
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                                                                  FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
                                                                                                    FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
                              FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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                  FILING DATE:
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/21547
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o. 6664376
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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PCT/US99/28565
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US-09-902-775A-119
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-119
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
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Patent No. 668645
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TITLE OF IN
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
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Local Similarity 26.5%;
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INVENTION:
   : Williams, P. Mickey
: Wood, William, I.
: Wood, William, I.
: NVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                             Stewart, Timo
                                                                             Roy, Margaret Ann
Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Godowski, Paul J.
Grimaldi, Christopher
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Filvaroff, Ellen
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Botstein, David
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Acids Encoding
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UR-09-397-243D-3
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LENGTH: 299
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PRIOR FILING DATE: 2000-01-05
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PRIOR TILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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CURRENT FILING DATE: 2001-07-10
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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PILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28313
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26.5%;
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APPLICANT: Kornecki, Elizabeth
APPLICANT: Sobocka, Malgorzata B.
APPLICANT: Sobocka, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERENCE: 011.00221
CURRENT: APPLICATION NUMBER: US/09/397,243D
CURRENT FILING DATE: 1999-9-16
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
SEQ ID NOS: 27
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SEQ ID NO
LENGTH: 299
TYPD: DET
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US-09-906-700-119
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GENERAL INFORMATION:
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Best Local Similarity
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Williams, P. Mickey
Wood, William, I.
VENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                                                Stewart, Timo
Tumas, Daniel
                                                                                                                Roy, Margaret Ann
                                                                                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
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Hillan, Kenneth, J.
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Grimaldi, Christopher
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Filvaroff, Ellen
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Botstein, David
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                                                                                              Timothy A.
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26.5%; Pred. No. 7e-10;
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
LENGTH: 299
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                      Human albumin fusion protein #1163. W0200177137-A1.
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Human gene 11 encoded secreted protein HMSOW51, SEQ
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Human secreted protein, SEQ ID;
W0200295010-A2.
28-NOV-2002.
(HUMA-) HUMAN GENOME SCI INC.—
Nery Match
Local Similarity 100.0%; So
                                                                ADL77754 standard;
Albumin fusion prot
US2004010134-A1.
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WO2003004622-A2.
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rry Match 100.0%;
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Albumin fusion protein related therapeutic protein
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WO2002102993-A2.
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(ROSE/) ROSEN C A.
(HASE/) HASELTINE W
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ry Match 100.0%;
Local Similarity 100.0%;
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15-APR-2004,
(GETH) GENENTECH INC.
(March 1971ty 100.0%;
                         Human gene 11 encoded secreted prote WO200136432-A2.
                                                                                                                                      AAY41691 standard; protein; 321
Human PRO 362 protein sequence.
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W02004031105-A2.
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Human B7-H6 protein
WO2004022594-A2.
AAB33429 standard; protein;
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Amino acid sequence of the PRO362 p
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(HELI-) HELIX RES INST.
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Human polypeptide, SEQ ID NO: 3986.
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100.0%; Score
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(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

Match 80.5%; St
                                                                                                                                                                                                                                                   ABU84879 standard; I
Human secreted and US2002177553-A1.
28-NOV-2002.
                                                      Human secreted/transmembrane US2003004102-A1.
02-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and tra. US2003050239-A1.
                                                                                                                                                                     ABU61077 standard; protein; 321
Human PRO362 polypeptide.
US2002169284-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO362 protein UNQ317 WO200053758-A2.
                                                                                                                                                  (GETH
                                                                                                                                                                                                                                                                                                                                                                 ABU72199 standard; protein; 321 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO362 pr
WO200053754-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO362 antitumour protein.
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Human PRO362 (UNQ317) prote
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14-SEP-2000.

(GETH ) GENENTECH INC.

80.5%;

80.5%;

100.0%;
            ABU07737
                                                                                                    ABU80346 standard; protein; 321 AA
                                                                                                                                                          14-NOV-2002
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                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB24047 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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-2002.
) GENENTECH INC.
80.5%; Sc
100.0%;
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standard;
33 related
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protein; 321 AA antigen PRO362.
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transmembrane po
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transmembrane
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Pred. No. 4.3e-137;
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Pred.
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Pred. No. 4.3e-137;
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. No. 4.3e-137;
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. No. 4.3e-137;
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.3e-137;
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1.3e-137;
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Best Loc
RESULT 41
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RESULT 40
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US2003083248-A1.
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US2003045462-A1.
06-MAR-2007
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Novel human secreted and transmembrane
US2003050240-A1.
                    Human secreted/transmembrane US2003054405-A1.
                                                                                                                                                                                          ADC61460 standard; protein; : Human secreted/transmembrane US2003049684-A1.
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| 19003
| GETH | GENENTECH INC.
| 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 19008 | 1900
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Human secreted/transmembrane polype
US2003055216-A1.
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Novel human secreted and transmembrane protein PRO362.
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                                                                ADC63424 standard;
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GETH ) GENENTECH INC.
80.5%;
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AR-2003.
AH ) GENENTECH INC.
80.5%; SC
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100.0%;
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Pred. No. 4
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. No. 4.3e-137;
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No. 4.3e-137;
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No. 4.3e-137;
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, 4.3e-137;
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4.3e-137;
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4.3e-137;
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.3e-137;
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RESULT 47
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RESULT
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Best Local Similarity
RESULT 51
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RESULT
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10-APR-2003.
(GETH ) GENENTECH INC.
(GETH ) B0.5%; S0
Watch "THY 100.0%;
ADC78883 standard; |
Human PRO protein #
WO2003034984-A2.
01-MAY-2003.
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                                                                                                                                                                                                           Human secreted/transmembrane US2003073624-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                ADC41093 standard; protein; 321 AA. Human secreted/transmembrane protein, US2003072745-A1.
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                                                                                                            Human secreted/transmembrane US2003104998-A1.
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                                                                                                   05-JUN-2003
                                                                                                                                      ADC41717 standard; protein;
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                                                                                                                                                                                                                                      ADC62084 standard; protein; 321 AA
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                                                                                    (GETH ) GENENTECH INC.
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Pred. No. 4.3e-137;
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Pred. No. 4.3e-137;
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Pred. No. 4.3e-137;
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GENENTECH INC

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RESULT 56
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RESULT 53
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30-OCT-2003...
(GETH) GENENTECH INC.
80.5%; Sc
Match 7-1ty 100.0%;
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                                     US2003206915-A1.
                                                ADG59969 standard; protein; :
                                                                                                                          Human secreted/transmembrane protein, US2003216561-A1.
                                                                                                                                                                                                                            Human secreted/transmembrane US2003195333-A1.
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Human secreted/transmembrane
US2003203433-A1.
30-OCT-2003.
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(GETH) GENENTECH INC.
80.5%;
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30-OCT-2003.
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(GETH ) GENENTECH INC.
80.5%;
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Pred. No. 4.3e-137;
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Best Local Similarity
RESULT 61
ID ADH62529 standard, p
DE Human PRO362 protein
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
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RESULT 64
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RESULT 63
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Best Local Similarity
RESULT 62
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Best Local Similarity
 Best Local Similarity
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                                ADF61127 standard; protein; 321 AA. Human secreted/transmembrane protein, US2003195345-A1.
16-OCT-2003.
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05-JUN-2003.
(GETH) GENENTECH INC.
80.5%;
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100.0%;
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Human secreted/transmembrane
US2003104536-A1.
05-JUN-2003.
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                      (GETH
                                                                                                           (WOOD/)
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GODOWSKI P J.
GIRMALDI J C.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
KTO G G
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GODDARD A.
GURNEY A L.
NAPIER M A.
TUMAS D.
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DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
                     GENENTECH
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PAONI N F.
ROY M A.
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STEWART T A.
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BAKER K P.
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Pred.
                                                                                     Score 1688; DB 8;
Pred. No. 4.3e-137;
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Pred. No. 4.3e-137;
 Score 1688; DB 8;
Pred. No. 4.3e-137;
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Pred. No. 4.3e-137;
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           Length 321;
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RESULT
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RESULT 73
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Human secreted/transmembrane
US2003204055-A1.
                                            ADP41067 standard; protein; 321 Human secreted/transmembrane pro US2003199435-A1.
23-OCT-2003.
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16-OCT-2003.
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23-OCT-2003:
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                                     Human secreted/transmembrane protein, US2003216305-A1.
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Human secreted protein #466
WO2002102994-A2.
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15-APR-2004.

(GETH) GENENTECH INC.

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Human STIGMA protein.
WO2004031105-A2.
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Human neurotrimin homologue
EP1386931-Al
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 ADA41415 standard;
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11-MAR-2004.
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Human

secreted

protein.

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Query Match
Best Local S
RESULT 101
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Best Local S
RESULT 99
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RESULT 96
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RESULT 95
                               Best Local Similarity
RESULT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 97
                                                      Query Match
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Best Local Similarity
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16-JAN 2003.
(HUMA-) HUMAN GENOME SCI INC.
21Y Match
73.7%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene 147 encoded secreted W0200276488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted p
WO2003038063-A2.
08-MAY-2003.
Human protein EP1396543-A2.
                                                                                        AAM93588 standard;
Human polypeptide,
EP1130094-A2.
                                                                                                                                                                         ADL67174 standard; protein; 2
Human B7-H6 (ECD) protein SEQ
WO2004022594-A2.
18-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB91804 standard; protein; Human secreted protein #SEQ WC2003004622-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR48114 standard; protein, Human secreted protein, WO200295010-A2.
                      ADL31354 standard;
                                                                    (HELI-)
                                                                              05-SEP-2001
                                                                                                                                                                                                                                                         12-AUG-1999
(HUMA-) HUM
                                                                                                                                                                                                                                                                               WO9940100-A1.
                                                                                                                                                                                                                                                                                        AAY30814 standard; protein; 306 AA.

Human secreted protein encoded from gene
                                                                                                                                                                                                                                                                                                                                                                       ADN35312 standard;
Human short STIgMA
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
ry Match 73.7%;
t Local Similarity 76.2%;
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27-DEC-2002.
                                                                                                                                      (CYTO-) CYTOS BIOTECHNOLOGY AG.
ry Match 70.5%; Score 1480;
t Local Similarity 100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC74547 standard; protein;
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ry Match 73.7%;
t Local Similarity 76.2%;
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                                                                                                                                                                                                                               Local Similarity
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R-2004.

A) GENENTECH INC.

73.7%; (76.2%;
                                                                   HELIX RES
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          dard; protein; 184 encoded by a full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein -
                                               $ INST.
46.9%;
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)tein, SEQ
                                                                                                    protein; 184 AA.
SEQ ID NO: 3387.
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73.7%;
76.2%;
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76.2%; 1
                                             100.0%;
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2 ID
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ID 1005.
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Pred.
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Pred. No. 6
         AA.
length
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NO:44.
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No. 6.
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No. 6.
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No. 6.2e-125;
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No. 6.1e-125;
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No. 6.1e-125;
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No. 6.1e-125
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            CDNA
                                             1.6e-76;
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.le-125;
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                                                                                                                                        DB 8;
.4e-119;
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            SeqID
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Best Local Similarity
RESULT 104
ID ADRIAGO
     Query Match
Best Local Similarity
RESULT 110
ID AAY23321 standard; po
DE Amino acid sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 108

ID AAE10596 stdndard; p.
DE Human macrophage exp
PN W0200164839-A2.
PD 07-SEP-2001.
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ID AUMAN
DE Human
PN US2003
PD 18-DEC
PA (TANG/
PA (LIUC/
PA (CHEN/
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Best Local Similarity 100.0%; Pred. No. 1.6e-76;

RESULT 103

ID AAY82322 standard; protein; 175 AA.

DE Human protein transport molecule (PTAM) SEQ ID NO:6.

PN W0200012703-A2.

PD 09-MAR-2000.

PA (INCY-) INCYTE PHARM INC.

PA (INCY-) INCYTE PHARM INC.

Query Match

Best Local Similarity 64.7%; Pred. No. 8.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.4%; RESULT 107
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Query Match 40.0%; Score 840;
Best Local Similarity 47.4%; Pred. No. 6
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RESULT 105
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                   (TANG/) TANG Y T.
(LIUC/) LIU C.
(ASUN/) ASUNDI V.
(CHEN/) CHEN R.
(OLAN/) QIAN X B.
(WANG/) WANG Z WANG J.
(ZHAN/) ZHANG J.
(ZHAN/) ZHANG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL67146 standard; protein; 188 AA.
Mouse B7-H6(ECD) protein SEQ ID NO:16.
W02004022594 A2.
18-MAR-2004,
19-MAR-2004,
19-YING BIOTECHNOLOGY AG.
19-YINGCH 29-2%; Score 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN35313 standard; protein; 280 AA Murine STIGMA protein. W02004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK70486 standard; protein; 175 AA.
Respiratory disease differentially expressed protein #52.
W02003101283-A2.
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AAY23321 standard; protein; 299 AA.
Amino acid sequence of the PRO301 polypeptide.
                                                                                                                                                                                                                                                                             ADH80723 standard, protein; 300 AA.
Human polypeptide #40.
US2003232054-A1.
18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human macrophage-expressed protein #21.
WO200164839-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE10596 standard; protein; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL67144 standard; protein; 280 AA. Mouse B7-H6 protein SEQ ID NO:14. WO2004022594-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE CORP.
                                                                                      DRMA/) DRMANAC R T.
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                                                                                                      ZHANG J.
ZHOU P.
CAO Y.
                                                    8.6%;
27.9%;
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98.9%;
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64.7%;
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Pred. No. 1.6e-44;
                                                  Score 180; DB 8;
Pred. No. 8.1e-07;
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Pred. No. 1.7e-34;
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Pred. No. 6.8e-64;
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                                                                      300;
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AB24405 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 AM2534 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 AM29534 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 AM29534 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 AM29534 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 Local Similarity 26.5%; pred. No. 1.1e-06 AB80232 standard; protein; 299 AA. Local Similarity 26.5%; pred. No. 1.1e-06 AB80232 standard; protein; 299 AA. Local PRO301 protein.	O4-NOV-1999. (GENE-) GENESIS RES & DEV CORP LTD. QUERY MATCH B.5%; SCOTE 178.5; DB BEST LOCAL Similarity 26.5%; Pred. No. 1.1e-06 SULT 116 AAY70670 standard; protein; 299 AA. Human PRO301 protein. W0200015797-A2. 23 -MAR-2000. (GETH) GENENTECH INC. B.5%; SCOTE 178.5; DB BEST LOCAL Similarity 26.5%; Pred. No. 1.1e-06 SULT 117	(GETH) GENENTECH INC. 8.5%; Score 178.5; DB Best Local Similarity 26.5%; Pred. No. 1.1e-06 SULT 114 AAY76011 standard; protein; 299 AA. Human A33 receptor homologue, SEQ ID NO:189. W09955865-A1. 04-NOV-1999. (GENE-) GENESIS RES & DEV CORP LTD. Query Match Best Local Similarity 26.5%; Pred. No. 1.1e-06 SULT 115 AAY76076 standard; protein; 299 AA. Human A33 receptor homologue, SEQ ID NO:331. W09955865-A1.	AY08071 standard; protein; 299 AA. Jaman RO307 protein. D991421-A2. SETH) GENENTECH INC. Y MATCh Local Similarity 26.5%; Score 178.5; DB LOCAL Similarity 26.5%; Pred. No. 1.1e-06 113 AY13364 standard; protein; 299 AA. AY13364 standard; protein PRO301. D9914328-A2. D9914328-A2.	W09927098-A2. 03-UUN-1999; (GETH) GENENTECH INC. B.5%; Score 178.5; DB Best Local Similarity 26.5%; Pred. No. 1.1e-06 SULT 111 AAW74464 standard; protein; 299 AA. F11 antigen protein sequence. W09902561-A1. 21-JAN-1999; (SMIK) SMITHKLINE BEECHAM CORP. 21-JAN-1999 (SMIK) SMITHKLINE BEECHAM CORP. DB Query Match Best Local Similarity 26.5%; Pred. No. 1.1e-06
:90. 5; DB 1.1e-0 1.1e-0	; DB	5; DB 1.1e-0 :189. :189. DB 1.1e-0	; DB	.1e-
Length Length	Length Length	Length Length	Length	Length Length
29 99;	299;	299;	299;	299;

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RESULT 121
ID AAB560
DE Skin c
RESULT 128
ID AAU144
DE Human
PN WO2001
PD 02-AUC
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RESULT 125
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Best Local Similarity
RESULT 120
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RESULT 126
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                                                                                                                                                               Human angiogenesis-associated protein PRO301, WO200053753-A2.
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Human polypeptide,
EP1130094-A2.
         Human novel protein WO200155437-A2.
                                                                                       Human novel protein WO200155437-A2.
                                                                                                         AAU14405 standard;
                                                                                                                                                                                                                                      AAU12354 standard; protein;
Human PRO301 polypeptide sec
WO200140466-A2.
07-JUN-2001.
                                                                                                                                                                                                                                                                                                                               Human immune response WO200119991-A1.
                                                                                                                                                                                                                                                                                                                                                   AAU00823 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           AAB31202 standard;
Amino acid sequence
WO200077037-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200069884-A2.
23-NOV-2000.
(GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB55950 standard;
Skin cell protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB56015 standard;
Skin cell protein,
WO200069884-A2.
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(HELI-) HELIX RES INST.
                              AAU14404 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH
                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                  (GETH ) GENENTECH INC.
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h 8.5%; Score 178.
Similarity 26.5%; Pred. No.
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n #276.
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e of human polypeptide
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SEQ ID NO: 189.
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SEQ ID NO: 331.
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SEQ ID NO: 3365.
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26.5%;
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26.5%;
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No. 1.1e-06;
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No.
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No.
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1.1e-06;
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Best Loca
RESULT 129
ID A***
                                                Query Match
Best Local S
RESULT 137
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RESULT 133
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Pry Match 8.5%;
St Local Similarity 26.5%;
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Human gene 23 encoded secret
WO200136440-A1.
                            ABB72215 standard; protein; Human protein isolated from
                                                                                                             ABG64552 standard; pi
Human albumin fusion
                                                                                                                                                                                    Human albumin fusion WO200177137-A1.
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Human polypeptide;
WO200190304-A2.
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                 Human protein i
WO200190357-A1.
                                                          (HUMA-) HUMAN GENOME SCI INC. ry Match 8.5%; t Local Similarity 26.5%;
                                                                                           18-OCT-2001
                                                                                                     WO200177137-A1.
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Human PRO301 prote;
WO200200690-A2.
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ry Match 8.5%;
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WO200136440-A1.
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23 encoded secreted protein
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US2003040014-Al.
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US2002192659-A1.
19-DPC-2000
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US2002146709-A1.
                                   ABU81052 standard; protein; Human PRO polypeptide #183.
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(GENE-) GENESIS RES
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US2002197671-Al.
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(GETH ) GENENTECH INC.
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US2003036180-Al.
20-FEB-2007
                           ABU64519 standard; protein; ;
Human secreted/transmembrane
US2002160374-A1.
31-OCT-2002.
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Novel secreted and
US2003017563-A1.
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Query Match
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RESULT 199
ID ADAB4738 standard; p:
DE Novel human secreted
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
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RESULT 194
ID ADA42300 standard; pi
DE Human secreted/transi
PN US2003054401-A1.
PD 20-MAR-2003.
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RESULT 198
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RESULT 196
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RESULT 193
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US2003073216-A1.
17-APR-2007
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Novel human secreted and transmembrane protein PRO301
US2003082695-A1.
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20-MAR-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembr.
US2003044945-A1.
06-MAR-2003.
(GETH) GENENTECH INC.
                   ADA84738 standard; protein; 299 AA. Novel human secreted and transmembrane protein PRO301 US2003082708-A1. 01-MAY-2003.
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Human secreted/transmembrane
US2003039969-A1.
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RESULT 236
ID ADB22848 standard;
DE Human PRO polypepti
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RESULT 229
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Human PRO polypeptide #183. US2003077711-Al.
                                                         US2003068793-A1.
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Human secreted/transmembrane protei
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US2003082686-A1.
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Human PRO polypeptide #183.
US2003059909-A1.
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DE Human secreted/transmembrane pp
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Human PRO polypeptide #183.
US2003082762-A1.
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US2003077712-A1.
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Human PRO polypeptide #183.
US2003082698-A1.
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US2003082697-A1.
01-MAY-2003.
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                 ADB35035 standard; protein; ;
Human PRO polypeptide SEQ ID
US2003077718-A1.
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Novel human.secreted and transmembrane
US2003082696-A1.
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GENENTECH INC.

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Query Match
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20-FEB-2003.
(GETH ) GENENTECU
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US2003082692-A1.
                             ADC28851 standard; protein; Human secreted/transmembrane US2003049677-A1.
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Human secreted/transmembrane
US2003036061-A1.
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             Novel human secreted and transmembrane US2003087366-A1.
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Novel human secrete
US2003092107-A1.
                                                                                                  Novel human secreted US2003087365-A1.
                                                                                                                      ADC52940 standard;
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Human secreted/transmembrane
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RESULT 274
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ID ADC60485 standard;
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RESULT 281
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US2003087362-A1.
                           Human secreted/transmembrane US2003082541-A1. 01-MAY-2003.
                                                                                                              ADC58517 standard; protein; 299 AA. Novel human secreted and transmembrane US2003087346-A1.
                                                                                                                                                                                 ADC55947 standard; protein; 299 Novel human secreted and transme US2003087360-A1.
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US2003087361-A1.
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US2003194774-A1.
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                                                 ADD10343 standard; protein; 299 AA. Human secreted/transmembrane PRO polypeptide US2003105011-A1.
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US2003087358-A1.
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Human secreted/transmembrane
US2003104381-A1.
05-JUN-2003.
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Human secreted/transmembrane
US2003104469-A1.
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US2003194771-A1.
ADD53060 standard; protein;
Human PRO polypeptide #183.
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US2003199055-A1.
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Human PRO polypeptide #183.
US2003199030-A1.
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Human PRO polypeptide #183.
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Novel human secreted and transmembrane protein PRO301
US2003203432-A1.
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Human PRO polypeptide
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Human PRO polypeptide #183.
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US2003203428-A1.
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US2003194791-A1.
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Human PRO polypeptide #183.
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PA (GETH) GENENTECH INC.

QUETY MATCH
BUET LOCAL Similarity 26.5%; i
RESULT 327

ID ADE32859 standard; protein; 25
DE Novel human secreted and trans
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
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RESULT 325
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RESULT 324
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RESULT 323
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RESULT 321
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RESULT 326
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RESULT 319
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Human PRO polypeptide #183.
US2003199025-Al.
23-OCT-2003.
(GET1) GENENTECH INC...
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Human PRO polypeptide #183.
US2003199026-A1.
23-OCT-2003:
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Human PRO polypeptide #183.
US2003199064-A1
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                                                                                                                                    ADD78909 standard; protein; 299 AA. Human PRO polypeptide #183. US2003203429-A1. 30-OCT-2003.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #183.
US2003199059-A1.
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Human PRO polypeptide #183.
US2003199033-A1.
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Human PRO polypeptide #183.
US2003194768-A1.
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Pred. No. 1.1e-06;
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Pred. No. 1.1
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ADF97492 standard; protei Human PRO polypeptide #18 US2003207370-A1. 06-NOV-2003. (GETH) GENENTECH INC. (GETH) 8.5	ADG23157 standard; proteinovel human secreted and US2003207384-A1. 06-NOV-2003. (GETH) GENENTECH INC. QUERY MATCH Best Local Similarity 26.5	ADG21516 standard; protei Novel human secreted and US200320735-A1. 06-NOV-2003. (GETH) GENENTECH INC. QUery Match B.5 Best Local Similarity 26.5 SULT 335	DE92807 standard; proteinan Pro polypeptide #18 S2003194777-Al. S-OCT-2003. SETH) GENENTECH INC. Match 8.5 Local Similarity 26.5	Human PRO polypeptide #1 US2003199034-A1. 23-OCT-2003. (GETH) GENENTECH INC. Query Match 8. Best Local Similarity 26. SULT 333	Human PRO polypeptide #18 US2003199031-A1. 23-OCT-2003. (GETH) GENENTECH INC. GEST Match Similarity 26.5 SULT 332 ADE04678 standard, protes	ADD89995 standard; prote Human PRO polypeptide #1 US2003199028-A1. 23-OCT-2003. (GETH) GENENTECH INC. Query Match 8 Best Local Similarity 26 SULT 331	ADD80567 standard; protei Human PRO polypeptide #18 US2003207418-A1. 06-NOV-2003. (GETH) GENENTECH INC. Query Match 8.5 Best Local Similarity 26.5	ADB42551 standard; protei Human PRO polypeptide #18 US2003199032-A1. 23-OCT-2003. (GETH) GENENTECH INC. Query Match 8.5 Best Local Similarity 26.5	cy Match Local Similarity 26.5
n; 299 AA. 3. 3. Score 178.5; DB 7;	n; 299 AA. transmembrane protein PR *; Score 178.5; DB 7; *; Pred. No. 1.1e-06;	rane protein 178.5; DB 7	n; 299 AA. 3. \$; Score 178.5; DB 7; \$; Pred. No. 1.1e-06;	יי יי	3. \$; Score 178.5; DB 7; \$; Pred. No. 1.1e-06; n; 299 AA.	, 299 , sco	n; 299 AA. 3. 3. \$; Score 178.5; DB 7; \$; Pred. No. 1.1e-06;	n; 299 AA. 3. 3. 4; Score 178.5; DB 7; 4; Pred. No. 1.1e-06;	<pre>%; Score 178.5; DB 7; %; Pred. No. 1.1e-06;</pre>
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(GURNY) GURNEY A L.
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(WOOD/) WOOD W I.
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US2003207372-A1.
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US2003207373-A1.
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Human secreted/transmembrane
US2003054352-A1.
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Novel human secreted and transmembrane
US200320739-A1.
06-NOV-2003.
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Human secreted/transmembrane
US2003039972-A1.
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Human secreted/transmembrane polypeptide PRO301
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US2003171568-A1.
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andard; protein; 299 AA. secreted and transmembrane
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Pred. No. 1.1
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No.
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No.
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No. 1.1e-06;
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No.
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1.1e-06;
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1.1e-06;
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Le-06;
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Let #183.

Lety Match
Best Local Similarity 26.5%; Pr
RESULT 359
ID ADD87915 standard; pro-
PN US200309211
PD 15-May
PA
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Best Local Similarity 26.5%;
BESULT 358
ID ADD76551 ståndard; protein; 2:
DE Human PRO pdlypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003 ;
PA (GETH) GENENTECH INC.
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ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301. PN US2003087357-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 26.5%; Pred.
RESULT 363
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/transmembrane protei
PN US2003129592-A1.
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Best Local Similarity
RESULT 360
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RESULT 357
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Best Local Similarity 26.5%;
RESULT 362
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Best Local Similarity
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US2003203440-A1.
O-CCT-2003.
                                                                                       ADE75767 standard; protein;
Human PRO polypeptide #183.
US2003211571-A1.
13-NOV-2003.
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Novel human secreted and transmembrane
US2003092115-A1.
15-MAY-2003.
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Human secreted/transmembrane
US2003130489-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
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              protein,
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ID ADE71382 standard; protein; 299 AA. ID ADE71382 standard; protein; 299 AA. DE Human secreted/transmembrane protein, #25. PN US2003148370-A1. PD 07-ANG-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 26.5%; Pred. No. 1.1e-0 RESULT 372 ID ADE18368 standard; protein; 299 AA. DE Human PRO polypeptide #183. PN US2003194794-A1. PD 16-OCT-2003.	941186 standard; protein; 299 AA. an secreted/transmembrane polypeptide 2003104558-A1. 2001.2003. 2TH) GENENTECH INC. 8.5%; Score 178.5; Match Match 0.0cal Similarity 26.5%; Pred. No. 1.	ADE89229 standard; protein; 299 AA. Human PRO polypeptide #183. US203199062-A1. 23-OCT-2003. (GETH) GENENTECH INC. 28-OCT 178.5; Duery Match Best Local Similarity 26.5%; Pred. No. 1.1e- SULT 370	ADD87363 standard; protein; 299 AA. Human PRO polypeptide #183. US2003203439-A1. 30-OCT-2003. (GETH) GENENTECH INC. 8.5%; Score 178.5; D ry Match t Local Similarity 26.5%; Pred. No. 1.1e-	224538 standard; protein; 299 AA. an PRO polypeptide #183. 200303211-A1. MAY-2003. TH) GENENTECH INC. 8.5%; Score 178.5; DB Occal Similarity 26.5%; Pred. No. 1.1e-0 168	233895 standard; protein; 299 AA. an PRO polypeptide #183. 2003092110-A1. MAY-2003. MAY-2003. STH) GENENTECH INC. 8.5%; Score 178.5; DB Match 8.5%; Pred. No. 1.1e-0	23343 standard; protein; 299 AA. Nan PRO polypeptide #183. 1003092108-A1. MAY-2003. MAY-2003. TH) GENENTECH INC. 8.5%; Score 178.5; DB Match Accal Similarity 26.5%; Pred. No. 1.1e-0	341304 standard; protein; 299 AA. an secreted/transmembrane PRO polypeptide 2003100497-A1. MAY-2003. ETH) GENENTECH INC. 8.5%; Score 178.5; DB Match Accal Similarity 26.5%; Pred. No. 1.1e-0	10-JUL-2003. (GETH) GENENTECH INC. 8.5%; Score 178.5; DB Juery Match BEST Local Similarity 26.5%; Pred. No. 1.1e-0 SULT 364
#25. 1.1e	de PRO	.5; 1.1e	.5; 1.1e	1.1e	1.1e-	.5; D	eptide .5; D	.5; D 1.1e-
Length	Length	Length	Length	Length	Length	Length	Length	Length
299;	299;	299;	299;	299;	299;	299;	299;	299;

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Query Match
Best Local Similarity 2
RESULT 381
ID ADE92255 standard; pro
DE Novel human secreted a
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
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RESULT 379
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RESULT 378
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RESULT 377
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RESULT 376
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Best Local Similarity 26.5%;
RESULT 373
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US2003199029-A1.
23-OCT-2003.
(GETH ) GENENTECH TWO
                  ADE92255 standard; protein; 299 AA. Novel human secreted and transmembr US2003199051-A1.
23-OCT-2003.
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US2003199060-A1.
23-OCT-7007
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Human PRO polypeptide #183.
US2003199054-A1.
23-OCT-2003.
(GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE91108 standard; protein;
Human PRO polypeptide #183.
US2003199061-A1.
23-OCT-2003.
C(GETH) GENENTECH INC.
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Human PRO polypeptide #183.
US2003199027-A1.
23-OCT-2003.
                                                                                                                                                US2003211569-A1.
                                                                                                                                                          ADE98505 standard; protein; 299 AA.
Human secreted/transmembrane protein, #25.
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Human PRO polypeptide #183.
US2003199052-A1.
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Pred.
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Pred. No. 1.1
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No. 1.1e-06;
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1.1e-06;
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ry Match ry Match ry Match ry Match ry Match r 189 ADG20138 standard; prote Alman PRO polypeptide #1 182003207376-A1. 16-NOV-2003. r 380 F 390 F 390	PRO polypeptide #11 207352-A1. -2003. GENENTECH INC. ch 8. 1 Similarity 26. 1 Similarity prote human secreted and	7 386 ### 3796 standard; prote Human secreted/transmemb US2003180312-A1. ### 25-SEP-2003. ### (GETH) GENENTECH INC. ### (CETH) GENENTECH 26. ### LOCAL Similarity 26. ### 187	I-DEC-2003. I-DEC-2003. SOBNOYERS L. SODO/) GODONRD A. SODO/) GODONSKI P J. SURN/) GURNEY A L. WATH/) MATHER J P. WILL/) WILLIAMS P M. WOOD/) WOOD W I. MATCh Local Similarity 26.	HU HU US 13 (G Query Best Best SULT SULT HU	3"7 62288B'	/ Match Local Similarity 2 382 382 382 382 383 383 383 Anthrity 2 20319363 A1. 5077-2003 5ETH) GENENTECH INC. / Match Local Similarity 2 383
5%; Score 178.5; DB 8; Lei 5%; Pred. No. 1.1e-06; in; 299 AA. 83. 5%; Score 178.5; DB 8; Lei 5%; Pred. No. 1.1e-06;	Score 178.5; DB 8; L Pred. No. 1.1e-06; 99 AA. smembrane protein PRO3	n; 299 AA. ane protein, #25. \$; Score 178.5; DB 8; I \$; Pred. No. 1.1e-06; n; 299 AA.	5%; Score 178.5; DB 8; Le:5%; Pred. No. 1.1e-06;	rane protein, #25. rane protein, #25. \$\frac{1}{5}\text{ Pred. No. 1.1e-06;} in; 299 AA. rane protein, #25.	in; 299 AA. transmembrane protein PRO 5%; Score 178.5; DB 8; 5%; Pred. No. 1.1e-06;	8.5%; Score 178.5; DB 8; Le (6.5%) Pred. No. 1.1e-06; Lein; 299 AA. #183. #183. 8.5%; Score 178.5; DB 8; Le (8.5%) Pred. No. 1.1e-06;
Length 299; Length 299;	ength 299; 01.	ength 299;	ngth 299;	ngth 299;	301. Length 299;	Length 299; Length 299;

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RESULT 396
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RESULT 395
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SULT 392
                 Query Match
Best Local
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US200320745-A1.
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US2003207375-A1.
06-NOV-2000
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US2003207351-Al.
06-NOV-2007
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US2003207422-A1.
                                                   ADF73372 standard; protein; 299 AA. Human secreted/transmembrane protein, US2003166051-A1.
                                                                                                                                                                                                                                                                    AUG16752 standard; protein;
Human PRO polypeptide #183.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO301.
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US200302331-A1.
30-JAN-2003
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                                                                                   ADH60491 standard; protein; 299 AA. Human secreted/transmembrane protein, US2004023331-A1.
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Novel human secret
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US2003207349-Al.
                               ADL77818 standard; protein; Albumin fusion protein relat US2004010134-A1.
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Human secreted/transmembrane
US200319611-A1.
09-OCT-2003.
                                                                                                                                                                                                        ADJ63577 standard; protein; 299 AA. Novel human secreted and transmembr US2004039164-A1.
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Human secreted/transmembrane
US2003096233-A1.
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Human platelet F11
US6699688-B1.
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02-OCT-2003.
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US2004058424-Al.
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26-FRR-200
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US2004043927-A1.
04-MAD-----
                                           ADO06154 standard; protein;
Human PRO polypeptide #21.
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Human PRO polypeptide #183.
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US2004010134-A1.
                                 Human PRO pol
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ry Match 8.5%; Score 178.5;
Local Similarity 26.5%; Pred. No. 1.1
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                                                                            .1e-06;
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RESULT 470
ID ADD35284 star*
DE Human pp^
PN WO2^
PD
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Best Local S
RESULT 472
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Best Local Similarity
RESULT 474
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Best Local Similarity
RESULT 473
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RESULT 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN35284 standard; prot
Human PRO301 protein.
WO2004031105-A2.
15-APR-2004.
(GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #183.
US2004077064-A1.
22-APR-2004
                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane US2004147017-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                ADR11006 standard; protein; 299 AA.
Human secreted/transmembrane protein, #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ95890 standard; protein; 2
T cell activation associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antipsoriatic protein sequence WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        US2004137561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN05140 standard;
                                                                                                                                                                                                                                                                                                                                       ADR17915 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                 EATON D L.
FERRARA N.
FILVAROFF E
                              WILLIAMS P N
                                                              PAONI N F.
ROY M A.
STEWART T A.
                                                                                                                                                      GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
                                                                                                                      GURNEY A L.
HILLAN K J.
KLJAVIN I J.
                                                                                                                                                                                                                                                                  ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
           Similarity
                                                                                                                                                                                       GERRITSEN M E.
                                                                                                                                                                                                   GERBER H.
                                                                                                                                                                                                               GAO W
                                                                                                           MATHER J P.
                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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          299
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1 protein #34.
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Pred.
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Pred.
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Pred. No. 1.1
          Score 178.5; DB 8; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                          protein,
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No. 1.1
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1.1e-06;

BB

Length

Length 299;

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RESULT 482
ID ADR465
DE Human
PN JP2004
PD 02-SEF
PA (DOXU-
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RESULT
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DE Hu
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RESULT 478
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  Best
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Best Local
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(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
31Y Match
8.5%; Score 178.5; DB 8;
51Y Match
8.5%; Pred. No. 1.1e-06;
                            AU2003259607-A1.
27-NOV-2003
                                                                                                                                                                                                                                                                                                                       Human JAM-1, F1
JP2004242513-A.
                                                                                                                                    ADT03591 standard; protein; 2
Human secreted/transmembrane
US2003152922-A1.
                                                                                                                                                                                                                               JP2004242513-A.
                                                                                                                                                                                                                                                      ADR46579 standard;
                                                                                                                                                                                                                                                                                                                                  ADR46573 standard; protein; 299 AA.
Human JAM-1, F11 receptor (F11R) transcript variant
                                                                                                                                                                                                                                                                                                                                                                                                                 ADR46571 standard; protein; 299 AA.
Human JAM-1, F11 receptor (F11R) transcript variant
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human JAM-1, F1:
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003207354-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI96350 standard; protein; 299 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR27641 standard;
Human F11 receptor
WO2004063327-A2.
                                                                                                                                                                                (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU S
ry Match 8.5%; Score 178.5; DB 8
t Local Similarity 26.5%; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR46577 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KORN/) KORNECKI E.
(BABI/) BABINSKA A.
(EHRL/) EHRLICH Y H
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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 Similarity
                       GENENTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein;
polypeptide #183.
                                                                                                                                                                                                                                          idard; protein; 299 I F11 receptor (F11R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; protein; 299 AA. receptor (F11R) transcript
                       INC.
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26.5%;
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No.
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1.1e-06;
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1.1e-06;
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Best
RESULT
          Best Local Similarity RESULT 491
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Best Local Similarity
RESULT 486
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                           Query Match
                                                                                                         Query Match
                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                         Novel protein; (useful for id WO2003054152-A2.
                                                        Human A33 antigen. WO9708189-A1.
                                                                                                                                   ADQ89964 standard;
Antagonist of cell
WO2004063362-A2.
                                                                                                                                                                                            03-JUL-2003.
(HYSE-) HYSEQ INC.
 AAY23323
                                                                           AAW14146 standard;
                                                                                                                                                                                                                                                                                             ADJ67616 standard; protein; Human ovarian specific poly; WO2004013311-A2.
                                                                                                                                                                                                                                                                                                                                                                                   ADE09073 standard; protein; 320 AA. Novel protein-related contig polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS74554 standard; protein; 2
Human secreted/transmembrane
US2004185531-A1.
                                      (LUDW-) LUDWIG INST
                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                           WO2003054152-A2.
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(GERR/
(GODD/
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WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOOD
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ROY M A.
STEWART T A.
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GODOWSKI P J.
GRIMALDI C J.
GRINEY A L.
HILLAN K J.
KLJAVIN I J.
KLJAVIN I J.
KATHER J P.
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BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
                                                                                              Similarity
                                                                                                                  CYCLACEL LTD.
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standard; protein; 319
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cycle progressi
                  CANCER F
8.4%;
27.5%;
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26.5%;
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26.5%;
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26.5%;
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26.5%;
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polypeptide :
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progression
                  RES.
Score
Pred.
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No.
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No. 1.1e-06;
                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                              polypeptide
                                                                                                                                                                                                                                                        3.5; DB 8;
. 1.3e-06;
                                                                                                                                                                                                                           genetic disorders)
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                                                                                                                                                                            .5; DB 7;
1.3e-06;
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                    DB 2;
                                                                                                DB 8;
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Query Match
Best Local S
RESULT 499
ID ADC78439
DE Human PRO
PN WO2000157
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                                                                                                                                                                                                                                                                                                                                                                                                                          (FONG/) FOND S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                    Cancer/angidgenesis/fibrosis-related WO2003042661-A2.
                                                                                                ABP62881 standard; protein;
Human polypeptide SEQ ID NO
                                                                                                                                                             WO2004039956-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA differentially expressed in US2002160387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB65863 standard;
Human A33 protein 9
WO200078808-A1.
 ADC78439 standard; protein; 299 Human PRO301 protein. WO200015796-A2.
                                                                                                                                                                                                                                                                    Human A33 antigen protein.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                         ADN35289 standard;
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US2003171568-A1.
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                                                               )7-MAR-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                    GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JONE/) JONES D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DH62533 standard;
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                                                                                                                                                                                                                                                                                                                                      EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MILL-) MILLENNIUM PHARM INC.
                                          Local Similarity
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                                                                                                                                              Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; protein; 319 AA. SEQ ID NO: 67.
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27.5%;
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27.5%;
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27.5%;
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SEQ ID NO:563.
                                                                                                  336 AA.
318.
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Pred.
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Pred.
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Pred.
                                                                                                                                                                                                                        Score 177; DB 8;
Pred. No. 1.6e-06;
                                           Score
Pred.
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Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 177;
Pred. No. 1
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Pred. No. 1.6e-06;
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                                           177;
No. 1.
                                                                                                                                177; DB 8;
No. 1.6e-06;
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No. 1
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No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                      polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer #43 product.
                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
1.6e-06;
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.6e-06;
                                           DB 5;
.7e-06;
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                                                                                                                                            Length 319;
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Best Loca
RESULT 504
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RESULT 502
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RESULT 501
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RESULT 505
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RESULT 503
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Best Local Similarity
RESULT 500
ID AAY08073 standard;
                                                                                    Query Match
Best Local Similarity
RESULT 506
            PA PA
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                                                                                                                                                                                                                                                                                         AAY08075 standard;
Human A33 protein i
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                              AAY23329 standard; protein; 273
An A33 related antigen sequence.
W09927098-A2.
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WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000.
(GETH ) GENENTECH INC.
                                         Human polypeptide #39.
US2003232054-A1.
18-DEC-2003.
                                                                                                                                                                                                      ADH62553 standard; protein;
Human A33 antigenic protein
US2003171568-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23327 standard; protein; 270 AA.
An A33 related antigen sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH62551 standard; protein;
Human A33 antigenic protein
US2003171568-A1.
                                                                          ADH80722 standard;
                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1999
                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO9927098-A2.
                                                                                                                                                                                                                                                                                25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                          GETH ) GENENTECH INC.
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) GODDARD A.
) GURNEY A L.
) NAPIER M A.
) TUMAS D.
) WOOD W I.
                                                                                                                ) GODDARD A.
) GURNEY A L.
) NAPIER M A.
) TUMAS D.
) WOOD W I.
TANG Y T.
LIU C.
ASUNDI V.
CHEN R.
                                                                                                                                                                        FONG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASHKENAZI A.
                                                                                                                                                                                  ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                    ; protein;
fragment #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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27.7%;
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27.7%;
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27.7%;
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26.5%;
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27.7%;
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27.7%;
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#2.
                                                                                                                                                                                                                                                                                                                                                                                                     273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 AA.
fragment #1.
                                                                          301 AA
                                                                                                                                                                                                                273 AA.
fragment #2
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Pred.
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Pred.
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Pred.
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Pred. 1
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Pred. No. 1
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No. 1
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No. 1.
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No. 1.
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No. 1.
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.5e-06;
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.6e-06;
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.6e-06;
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.5e-06;
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.5e-06;
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RESULT 511
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RESULT 508
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RESULT 507
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(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
                                                                                                                          Human DNA40628 protein fragment #2. WO9914241-A2.
                                                                                                                                                                                     AAY23328 standard; protein; 263 AA.
An A33 related antigen sequence.
W09927098-A2.
03-JUN-1999.
GETH) GENENTECH INC.
                                                      ADH62552 standard; protein; 263 P
Human PRO301 protein fragment #2
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                         ADH62550 standard; protein; 26 Human PRO301 protein fragment US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY08072 standard; protein;
Human DNA40628 protein.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2004.
(UYNY ) UNIV NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK40854 standard;
Human A33 molecule
US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An A33 related antigen sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23326 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999
                                                                                                             GETH ) GENENTECH INC.
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) GODDARD A.
) GURNEY A L.
) NAPIER M A.
) TUMAS D.
) WOOD W I.
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ZHOU P.
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                                    ASHKENAZI A.
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26.1%;
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26.1%;
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26.1%;
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26.1%;
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26.4%; Pred. No.
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nt #1.
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No. 5.4
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No.
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No.
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No.
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5.3e-06;
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3e-06;
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                                                                                   7.4e-06;
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Best Loca
RESULT 515
                                                                  Best Local Similarity RESULT 521
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Best Local Similarity
RESULT 519
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                                                                                         Query Match
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11-JUN-1998.

(HOFF) HOFFMANN LA ROCHE & BOS; ery Match 8.0%; 24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-SEP-2004.
02-SEP-2004.
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU
8.0%; Score 168
ery Match
24.8%; Pred. No.
                                                                                                                                                                                                           Mouse junction adhesion molecule US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW61379 standard; protein;
Human junctional adhesion mc
WO9824897-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR46581 standard; protein; Mouse junctional adhesion mc JP2004242513-A.
                               ABB83928 standard;
pCAR SEQ ID NO 4.
US2002059654-A1.
                                                                                                                Human JAM protei
WO2004031105-A2.
15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                   ADH62537 standard; protein; Murine JAM protein used in tUS2003171568-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse junctional adhesion molecule WO9824897-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE & Pry Match 8.0%; t Local Similarity 24.8%;
                                                                                                                                                  ADN35293 standard;
                                                                                                                                                                                                VIND (ANAM)
                                                                                                                                                                                                                                             ADK40853 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A33 related antigen WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY23325 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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                                                                                                     (GETH ) GENENTECH
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                                                                                                                                                                        Local Similarity
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GURNEY A L.
NAPIER M A.
TUMAS D.
BUHLER T.
GADIENT R
                                                                                                                                                                                                                                                                                         WOOD W I.
                                                                                                                                                                                                                                                                                                                                                   ASHKENAZI A. FONG S.
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                                                                                                                                       protein.
                                                                                                                                                                       NEW YORK STATE 8.0%; llarity 24.8%;
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                                                       protein;
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                                                                              8.0%;
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24.8%;
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24.8%;
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26.1%;
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Score 167; I
Pred. No. 1.
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Score 167; DB 2;
Pred. No. 1.1e-05;
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Score 167; DB 8;
Pred. No. 1.1e-05;
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Pred.
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Pred.
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Pred.
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Pred.
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No. 1.
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No. 1.
                                                                              167; DB 8;
No. 1.1e-05;
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No. 5.4e-06;
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.1e-05;
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.1e-05;
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Query Match
Best Local S
RESULT 530
ID ABB95562
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RESULT 526
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RESULT 525
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RESULT 523
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                                              ABB84956 standard; protein;
Human PRO5723 protein sequen
WO200200690-A2.
03-JAN-2002.
                                                                                                                               AAB65294 standard; protein; 352
Human PRO5723 protein sequence S
WO200073454-A1.
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Human PRO5723 protein.
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Gene 15 human secreted prote
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Mouse A33 antigen.
WO9708189-A1.
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Human RGS11 protein.
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ABB95562 standard; protein;
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(GADI/) GADIENT R A.
(KORN/) KORN R.
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RESULT 531
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                                                                                                                                               ABU80846 standard; protein;
Human PRO polypeptide #108.
US2003036635-A1.
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ABU14000 standard;
Human PRO5723 poly;
US2002103125-A1.
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US2003045687-A1.
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(GETH) GENENTECH INC.
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(GETH ) GENENTECH
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MARSTERS S A.
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GODDARD A.
GODOWSKI P J.
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polypeptide.
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                                             Novel human secreted and transmembrane US2003017476-A1.
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Human PRO5723 protein.
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                  Human secreted/transmembrane US2003054359-A1.
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Human secreted and
US2002197615-A1.
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Human PRO5723 poly
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Human secreted/transmembrane
US2003059831-A1.
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Human PRO5723 prot
US2003050448-A1.
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Human PRO5723 polyp
US2003017981-A1.
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ADB84837 standard; protein;
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ADC49966 standard; protein;
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Human secreted/transmembrane
US2003049681-A1.
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Human PRO polypeptide #141.
US2003045463-A1.
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US2003105290-A1.
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US2003100708-A1.
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US2003100715-A1.
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ADD74671 standard; protein;
Human PRO polypeptide #108.
US2003100713-A1.
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Novel human secreted and transmembrane
US2003100725-A1.
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US2003100724-A1.
29-MAY-2003.
                           ADG11346 standard; protein; 352 AA. Novel human secreted and transmembrane US2003096967-A1.
22-MAY-2003.
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Novel human secreted and tra
US2003096959-A1.
22-MAY-2003.
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Human PRO5723 polypeptide.
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US2003224984-A1.
04-DEC-2003.
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Human secreted/transmembrane
US2003219856-A1.
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RESULT 678
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Best Local Similarity
RESULT 677
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RESULT 675
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Best Local Similarity
RESULT 673
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Best Local Similarity
RESULT 671
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US2004044180-A1.
04-MAR-200
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK83058 standard; protein;
Human PRO polypeptide #140.
US2004043927-A1.
                                                                                                                                                                                                                                                         Human coxeackievirus WO9833819-A1.
                                                                                                                L9-MAR-1998.
(DAND ) DANA FARBER CANCER INST INC.
ry Match 7.6%; Score 1
ry Match 23.2%; Pred. N
                                                                                                                                                                                                          Jo-AUG-1990
(UYNY) UNIV NEW YORK STATE.

ry Match 7.6%;

r Local Similarity 23.2%;
                                                                                                                                                                                                                                                                   AAW69697 standard; protein; :
Human coxsackievirus and Ad2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH69776 standard; protein;
Human PRO polypeptide #108.
US2004019183-A1.
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                           Socation 2001.
2-JUN-2001.
(UYTE-) UNIV TECHNOLOGY CORP.
TY Match 7.6%;
Pry Match 23.2%;
                                                                                                                                                                             AAW57212 standard; protein; 365 AA.
Human coxsackievirus and adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI29937 standard; protein; 352 AA. Novel human secreted and transmembrane US2003096961-A1.
 ABB08040 standard; protein; 365 AA.
Human coxsackie-adenovirus receptor
                                                                                           Human CAR.
                                                                                                  AAB47270 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2004
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                                                                             JS6245966-B1.
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23.2%;
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                                  Score 159; DB 4; Pred. No. 7e-05;
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No. 7e-05;
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  (CAR).
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                                                                                                                        7e-05;
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.6e-05;
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.6e-05;
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.6e-05;
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Best Loca
RESULT 684
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Best Local Similarity
RESULT 687
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Best Local Similarity
RESULT 685
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Best Local Similarity
RESULT 683
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RESULT 680
Best Local Similarity RESULT 688
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Human CAR wild-type |
WC2003070915-A2.
28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BEC/LEC-related protein; 365 AA.
W02003080640-A1.
02-0CT-2003.
                                                                                                                                                                                                                                     Human PRO363 protein UNQ318 WO200053758-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
7.6%; Score 159; DB 5;
7.0%; Match
7.6%; Pred. No. 7e-05;
                                                      AAU12365 standard; protein; 373 AA Human PRO363 polypeptide sequence. WO200140466-A2.
                                                                                                                                                              AAB44248 standard; protein; 373 AA.
Human PRO363 (UNQ318) protein sequence
                                                                                                                                                                                                                                                                                                                                                    AAY41692 standard;
Human PRO 363 prote
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU12046 standard; protein; 505 AA. Human NOV4a CG59871-01 protein SEQ W0200281625-A2.
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ry Match 7.6%; Score 159;
t Local Similarity 23.2%; Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast can W02003000012-A2.
                                   (GETH
                                               07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ37063 standard;
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                                                                                                                                                     WO200053756-A2.
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                                                                                                                                                                                                                                                                                                                                            WO9946281-A2.
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                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  standard; protein; 373 AA.
363 protein sequence.
                                   INC.
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23.2%;
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e protein.
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r / ovarian cancer
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22.2%;
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22.2%;
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SEQ ID NO:87
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No.
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No.
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                       158.5;
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No. 7e-05;
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7e-05;
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             7.9e-05;
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AAB48146

standard;

protein;

373 AA

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RESULT 689
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RESULT 692
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03-JAN-2002.
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                                                                                                            WO200208284-A2.
                                                                                                                   Human angiogenesis
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Human A236 protein
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                                                                                                                           ABB95454 standard;
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WO200069885-A2.
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(MILL-) MILLENNIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB48108 standard; protein;
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                        MARS/
                                                                                     BAKE/)
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                      GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                        PAN Y.

BARNES T M.

FRASER C C.

WRIGHTON N.

MYERS P S.

KINGSBURY G.
                                                                                                                                                                                                        HOLTZMAN D. SHARP J D. LEIBY K R. BOSSONE S.
PAONI N F.
STEPHAN J F.
                 PAN
                                                                     GERBER H.
                                                                             FERRARA N.
                                                                                     GENENTECH INC. BAKER K P.
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related |
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22.2%; I
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Seq ID No
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22.2%;
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sequence SEQ
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Pred. No. 7.9
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No.
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No. 7.9e-05;
                                                                                                                     PRO363
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No. 7.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                         3.5; DB 4;
. 7.9e-05;
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Best Local S
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RESULT 701
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RESULT
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RESULT 703
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RESULT
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RESULT 695
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RESULT 697
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US2003032156-A1.
                                                                                                                                                                                      ABO25194 standard; protein; 373 AA.
Novel human secreted and transmembrane
US2003050239-A1.
                                                                                                      Novel human secreted and transmemts US2003045687. **
                                                                                                                                                                                                                                                              Human PRO polypeptide #65.
US2003036635-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                         Human secreted/transmembrane US2002160384-A1.
          US2002103125-A1.
01-AUG-2002.
                            ABU13999 standard; protein;
Human PRO363 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane US2003032023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU59186 standard; protein; Novel human secreted or trainus2002132252-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU58108 standard; protein;
Human PRO polypeptide #140.
US2003027163-A1.
                                                                                   (GETH
                                                                                                     US2003045687-A1.
                                                                                                                                                                  (GETH ) GENENTECH
                                                                                                                                                                                                                                                                                              ABU80803 standard;
                                                                                                                                                                                                                                                                                                                                                                                 ABU60617 standard; protein;
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                                                                                       Novel human secreted and transmembrane US2003068796-A1.
         US2003082704-A1.
01-MAY-2003.
                       ADB27937 standard; protein;
Human PRO polypeptide #194.
                                                                                                                                                                          Homo sapiens.
US2003049816-A1.
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Human PRO polypeptide #194.
US2003054517-A1.
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Human PRO polypeptide #194.
US2003073212-A1.
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Human PRO363 polypeptide.
US2003017981-A1.
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26-DEC-2002.
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Human secreted and
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US2003082693-A1.
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US2003068794-A1.
10-APR-2003.
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Human PRO polypeptide #194.
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US20308F351-A1.
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US2003082705-A1.
ADB18837 standard; protein; 373 AA. Novel human secreted and transmembrane US2003073211-A1.
                                                                                                                                     ADA24598 standard; protein; 373 AA. Novel human secreted and transmembr US2003050241-A1.
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US2003087349-A1.
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protein

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Best Local Similarity
RESULT 759
ID ADB24747 standard; F
DE Human PRO polypeptid
PN US2003077713-A1.
PD 24-APR-2003.
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Best Local &
RESULT 758
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RESULT 754
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Best Local Similarity
RESULT 757
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RESULT 753
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US2003068798-A1.
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US2003050240-A1.
  Human PRO polypeptide SEQ II
US2003077713-A1.
24-App-2000
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                                                                                                                                         ADA94719 standard; protein; 3
Human secreted/transmembrane
US2003059832-A1.
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US2003082710-A1.
01-MAY-2007
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(GETH ) GENENTECH INC.
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No. 7.9e-05;
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No. 7.9e-05;
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                                           7.9e-05;
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Best Local Similarity 22.2%; RESULT 765
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Query Match
Best Local Similarity 22.2%;
RESULT 764
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RESULT 760
                                                      Query Match
Best Local Similarity
RESULT 767
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Best Local Similarity
RESULT 766
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     Best
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Best Local :
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Human PRO polypeptide #194.
US2003082703-AI.
01-MAY-2003.
(GETH ) GENENTECH INC.
10-MAY-2004.
10-MAY-2005.
10-MAY-2004.
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17-APR-2003.
(GETH) GENENTECH INC.
(GETH) 7.6%; §
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                                                                                                    ADA47011 standard; protein;
Human PRO polypeptide #194.
US2003073210-A1.
                                                                                                                                                                                                                                                            ADA38944 standard; protein; 373 AA. Human secreted/transmembrane protein US2003059780-A1.
27-MAR-2003.
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Human PRO polypeptide #194.
US2003082761-A1.
01-MAY-2003.
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Novel human secreted and transmembrane protein PRO363.

US2003082708-A1.

01-MAY-2003.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO363.
US2003082695-A1.
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Human PRO polypeptide #194.
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                                                GENENTECH INC.
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Pred.
Score 158.5; DB 6; Pred. No. 7.9e-05;
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No. 7.9e-05;
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No. 7.9e-05;
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Human PRO polypeptide #194.
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US2003082762-Al.
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           Novel human secreted and transmembrane US2003069397-Al.
                                                                                         ADB47136 standard; protein; 373 AA. Novel human secreted and transmembrane US2003082687-A1.
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US2003088067-A1.
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US2003082692-A1.
          US2003064407-A1.
03-APR-2003.
                         ADC68655 standard; protein; 3 Human secreted/transmembrane
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Human secreted/transmembrane
US2003054986-A1.
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(GETH ) GEN
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Novel human secreted and transmembrane
US2003088072-A1.
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Novel human secreted and transmembrane
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US2003087362-A1.
08-MAY-2003.
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US2003087346-Al.
08-MAY-2003
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                            ADC14803 standard; protein; 373 AA. Novel human secreted and transmembrane US2003082546-A1.
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US2003087364-A1.
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Novel human secreted and transmembrane
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ADC47202 standard; protein; 373 AA.

protein PRO363

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US2003096972-A1.
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                                                                                              ADD07802 standard; protein; 373 AA. Novel human secreted and transmembrane
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US2003068623-A1.
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US2003194771-A1.
16-OCT-2003.
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US2003092103-A1.
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US2003059833-A1.
27-MAR-2003
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Human PRO polypeptide #194.
US2003194774-A1.
16-OCT-2003.
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US2003203438-A1.
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US2003194779-A1.
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US2003207372-A1.
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Human PRO polypeptide #140.
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Novel human secreted and transmembrane protein PRO363
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
US2003207377-A1.
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ADE21004 standard;
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US2003100722-A1.
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Human PRO polypeptide #65.
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Human PRO polypeptide #65.
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Novel human secreted and transmembrane
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29-MAY-2003.
(GETH ) GENENTECH INC.
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ADD87937 standard; protein;
Human PRO polypeptide #194.
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(GETH ) GENENTECH INC.
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US2003100711-A1.
29-MAY-2007
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US2003211571-A1.
13-NOV-2007
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US2003203440-A1.
ADE21250 standard; protein; Novel human secreted and tr. US2003100736-A1.
                                                                     ADE23365 standard; protein;
Human PRO polypeptide #194.
US2003092108-A1.
                                                                                                                                     ADE41314 standard; protein; 373 AA. Human secreted/transmembrane PRO po US2003100497-A1.
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15-MAY-2003.
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US2003100718-A1.
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                                                                                    ADE23917 standard; protein;
Human PRO polypeptide #194.
US2003092110-A1.
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US2003100732-A1.
ADE24560 standard; protein;
Human PRO polypeptide #194.
US2003092111-A1.
15-MAY-2003.
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                                                                                                                                                                          ADD85561 standard; protein; 373 AA. Novel human secreted and transmembr
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Human PRO polypeptide #65.
US2003100709-A1.
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US2003100796-A1.
29-MAY-2007
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Human PRO polypeptide #194.
US2003194794-A1.
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Novel human secreted and transmembrane
US2003100731-A1.
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Human PRO polypeptide #194.
US200319962-A1.
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Novel human secreted and transmembrane
US2003100719-A1.
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Human PRO polypeptide #65.
US2003100714-A1.
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Human PRO polypeptide #194.
US2003203439-A1.
                     ADE88699 standard; protein;
Human PRO polypeptide #194.
US2003199054-A1.
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No. 7.9e-05;
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Query Match
Best Local Similarity
RESULT 1010
ID ADFORM
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RESULT 1015
ID ADD74585 standard;
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Best Local Similarity
RESULT 1014
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Best Local Similarity
RESULT 1013
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Best Local Similarity
RESULT 1011
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                                                                              Human PRO polypeptide #65. US9003100710-A1. 29-MAY-2003.
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                                                                                                                                                                                                                                                            ADD77857 standard; protein; 373 AA. Novel human secreted and transmembrane US2003100730-A1.
29-MAY-2003.
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ADD74585 standard; protein;
Human PRO polypeptide #65.
US2003100713-A1.
29-MAY-2003.
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STEWART T A.
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HILLAN K J.
KLJAVIN I J.
KUO S S.
NAPIER M A.
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EATON D L.
FERRARA N.
FILVAROFF E.
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GIRMALDI J C.
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BAKER K P.
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Query Match
Best Local Similarity 22.2%; Pred. Nc
RESULT 1024
ID ADES1130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
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RESULT 1021
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23-OCT-2003.
(GETH ) GENENTECH INC.
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US2003199027-A1.
23-OCT-2003.
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Human secreted/transmembrane protein, PRO363.
US2003195345-A1.
16-OCT-2003.
(GETH) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO363.
US2003100716-A1.

29-MAY-2003.
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16-OCT-2003.
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Human PRO polypeptide #65.
US2003100723-A1.
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ecreted/transmemb 99436-A1. 2003. GENENTECH INC. h Similarity 22.	23-OCT-2003. (GETH) GENENTER Query Match Best Local Similar: SULT 1033 ADF26844 standa	1032)F34962 standard; proman PRO polypeptide 22003199029-A1.	PD 16-OCT-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 22.	ID ADF33377 standard; protein; 37 DE Human secreted/transmembrane p PN US2003194780-A1.	Query Match 7. Best Local Similarity 22.	ID ADF23394 standard; protein; 37 ID ADF23394 standard; protein; 37 DE Human secreted/transmembrane pN US2003203402-A1. pD 30-OCT-2003. pp 30-OCT-2003.	i an Ki	ADF40450 standard; prote Human secreted/transmemb US2003199021-A1.	TH) GENENTECH INC. Match Cocal Similarity 22.	724018 standard; paran secreted/trans	TH) GENENTECH INC. Match 7ocal Similarity 22.	193381 standard; pro han PRO polypeptide 1903199060-A1.	(GETH) GENENTECH INC. Query Match 7. Best Local Similarity 22. SULT 1027	ADE95271 standard; prote Human PRO polypeptide #1 US2003199052-A1.	Query Match Best Local Similarity 22.	35629 standard; prot nan PRO363 polypeptic 2003194760-A1.	Query Match Best Local Similarity 22. SULT 1025
score 158.5; pred. No. 7.9e	Score 158.5; Pred. No. 7.9e	n, 373 AA. 4.	core 158.5; red. No. 7.9e	3 AA. Protein, PRO36	core 158.5; red. No. 7.9e	in; 373 AA. brane protein, PRO36	core 158.5; red. No. 7.9e	in; 373 AA. rane protein, PRO36	6%; Score 158.5; 2%; Pred. No. 7.9e	rotein; 373 AA. membrane protein, PRO36	.6%; Score 158.5; .2%; Pred. No. 7.9e	tein; 373 AA. #194.	6%; Score 158.5; 2%; Pred. No. 7.9e	ein; 373 AA. 194.	6%; Score 158.5; 2%; Pred. No. 7.9e	in; 373 AA.	6%; Score 158.5; 2%; Pred. No. 7.9e
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Query Match
Best Local Similarity
RESULT 1037
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US2003199051-A1.
                               Human secreted/transmembrane US2003195344-A1. 16-OCT-2003.
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Human secreted/transmembrane protein,
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US2003207376-A1.
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US2003207352-A1.
06-NOV-2000
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US2003096962-A1.
                                                Novel human secreted and transmembrane US2003207426-A1.
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Novel human secreted and transmembrane
US2003096959-A1.
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Human PRO363 polypeptide.
US2003228655-A1.
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                                                   Novel human secreted and transmembrane US2003207424-A1. 06-NOV-2003.
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US2003207353-A1.
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US2003207359-A1.
06-NOV-2007
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US2003207351-A1.
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Human PRO polypeptide #194.
US2003207357-A1.
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22-MAY-2003.
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(GETH ) GENENTECH INC.
ADG15564 standard; protein;
Human PRO polypeptide #194.
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US2003207371-A1.
06-NOV-2003.
                                                                                ADG07218 standard; protein; 373 AA.
Novel human secreted and transmembrane
US2003207350-A1.
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Human PRO polypeptide #194.
US2003207374-A1.
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ADG07770 standard;
Novel human secrete
US2003207356-A1.
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US2003207423-A1.
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Novel human secrete
US2003207389-A1.
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Query Match
Best Local Similarity
RESULT 1079
ID ADG58577 standard; p
DE Novel human secreted
PN US2003207368-A1.
PD 06-NOV-2003.
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US2003207358-A1.
06-NOV-2003.
                                                                                            ADG55817 standard; protein; 373 AA.
Novel human secreted and transmembrane
US2003207365-A1.
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US2003096966-A1.
22-MAY-2003
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                   Human PRO polypeptide #194. US2003077723-A1. 24-App-2007
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US2003207420-A1.
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Human secreted/transmembrane protein, PRO363.
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                                                                                                                               Human secreted/transmembrane US2004005312-A1. 08-JAN-2004.
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Human secreted/transmembrane
ADG58800 standard; protein;
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Human PRO polypeptide #194.
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US2003207429-A1.
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Human PRO polypeptide #194.
US2003207361-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein
US2004009548-A1.
15-JAN-2004.
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EP1386931-A1.
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US2003096960-A1.
22-MAY-2007
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Novel human secreted and tra
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RESULT 1117
ID ADI14723 standard; p
DE Novel human secretee
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US200403836-Al.
26-FFR-2004
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ADJ65616 standard; protein;
Human PRO polypeptide #194.
US2004038335-A1.
                                                                               ADK66606 standard; protein;
Human PRO polypeptide #65.
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US2003207349-A1.
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15-JAN-2004.
(GETH ) GENENTE
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7.9e
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                                                                                                             .5; DB 8;
7.9e-05;
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.9e-05;
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Best Local Similarity
RESULT 1134
ID AD196372 standard; p
DE Novel human secreted
PN US2003207354-A1.
PD 06-NOV-2003.
                                                                                                                            Best Local Similarity RESULT 1133
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1130
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RESULT 1126
ID ADM27752 standard;
                                                                                                                                                                                                                Best Local Similarity RESULT 1132
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Best Local Similarity
RESULT 1129
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                                                              Query Match
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US2004077064-A1.
22-APP-2007
                                                                                                                                                                                                                                                                                                                                                 Antipsoriatic protein sequence #858 W02004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #194. US2004048333-A1.
                                                                                            ADI95820 standard; protein;
Human PRO polypeptide #194.
US2003077659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADM42476 standard; protein;
Human PRO polypeptide #194.
US2004058424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted/transmembrane US2004063921-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM17058 standard; protein; Human secreted/transmembrane US2004048332-A1.
                                                                                                                                                                                  EP1416279-A1.
                                                                                                                                                                                        ADO36720 standard; protein;
Human UKW polypeptide, SEQ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL06892 standard;
                                                                                                                                    (HOFF) HOFFMANN LA ROCHE & CO AG F.

Ty Match
7.6%; Score 158.5; DB 8;
Local Similarity 22.2%; Pred. No. 7.9e-05;
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) GENENTECH INC.
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                 andard; protein; 373
secreted and transme
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22.2%;
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22.2%;
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                     transmembrane
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) ID NO:2.
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No.
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7.9e-05;
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7.9e-05;
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7.9e-05;
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7.9e-05;
                    protein
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7.9e-05;
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Query Match
Best Local Similarity
RESULT 1135
ID ADAFATT
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RESULT 1142
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Best Local Similarity
RESULT 1141
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Best Local Similarity
RESULT 1137
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RESULT
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Best Local Similarity
RESULT 1138
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RESULT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ITOH/) ITOH A.
(HANA/) HANAZONO )
(OKAD/) OKADA T.
(OZAW/) OZAWA K.
                                       AAW82731 standard; protein; 397 AA. Adenovirus pACSG2SCAR.sig chimeric W09854346-A1.
                                                                                                                        AAB48145 standard;
Human A236 variant
WO200069885-A2.
                                                                                                                                                                                                         AAU83699 standard;
Human PRO protein,
WO200208288-A2.
                                                                                                                                                                                                                                                                                                                                                                            AAW82729 standard; protein;
Adenovirus pACTSG2-SCAR prot
WO9854346-Al.
                                                                                                                                                                                                                                                                       03-DEC-1998.
(GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                           Adenovirus SCAR.RGD
WO9854346-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human CAR/mouse anti-CD34
US2003092068-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CAR/mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                 AAW82730 standard;
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                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l2-FEB-2004.
(DIAD-) DIADEXUS INC.
                                                                                                                                                                                      GETH ) GENENTECH INC.
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(HANA/) HANAZONO Y.
(OKAD/) OKADA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-MAY-2003
 Local Similarity
                                                                                                                                                                                                                                                   Local Similarity
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                    GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           OZAWA
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                                                                                                                                                                                                                     protein;
Seq ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 412 AA.
F fusion protein.
                                                                                                                                  protein; 373 AA.
1 polypeptide.
                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                      protein
                                                                                7.5%;
22.2%;
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22.2%;
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25.9%;
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24.8%;
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25.9%;
7.5%;
25.9%;
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23.7%;
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polypeptide
                                                                                                                                                                                                                                                                                                                                                                                     ein; 264 AA.
Protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; 493 AA.
antibody
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                                                                                                                                                                                                                      290 AA.
lo 216.
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Pred. No.
                                                                                Score 156.
Pred. No.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 9.2e-05;
No.
                                                                                                                                                                                                                                                   156.5; DB 2;
No. 7.7e-05;
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No.
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No.
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No.
6.5; DB 2
. 0.00013;
                                                                                 0.00012;
                                                                                                                                                                 .5; DB 5;
8.3e-05;
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0.00014;
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7.9e-05;
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.9e-05;
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          Length 397;
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Query Matc
Best Local
RESULT 1147
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Best Local S
RESULT 1146
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ID ADASO17
DE Human C
PN US20030
PD 15-MAY-
PA (ITOH)
PA (OXAD)
PA (OXAD)
PA (OZAW)
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Best Local S
RESULT 1148
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Best Local Similarity
RESULT 1149
                         Query Match
Best Local Similarity
RESULT 1150
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RESULT 1145
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                                                                                                                                                                                                                                                                                          (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                     ADA54925 standard;
Human protein, SEQ
EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                                            Human prostatic carcinoma derive WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic prote w200175067-A2.
                                                                                                           ABP60991 standard; p
Novel human protein.
WO200250105-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostatic of WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CAR/SCF fur
US2003092068-A1.
                                                                                                                                                                                (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR66297 standard; protein; 358 AA.
Human prostatic carcinoma derived protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC. ry Match 7.4%; t Local Similarity 22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB48147 standard; protein; 373 AA.
Human A236 variant 3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HANA/) HANAZONO Y.
(OKADA) OKADA T.
(OZAW/) OZAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA50170 standard;
ADJ70089 standard; protein; 5636 AA.
Human heat mitochondrial protein as a therapeutic target SeqID1895.
                                                                                                                                                                                                         9-MAR-2003
                                                                       SMIK ) SMITHKLINE BEECHAM CORP. SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                             HINZ/) HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                       Local Similarity
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                                 GLAXO GROUP LTD.

7.4%;
h
7.4%;
Similarity 23.8%;
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n. SEQ ID
                                                                                                                                                          7.4%;
23.8%;
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24.38;
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23.1%;
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23.1%;
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25.9%;
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protein #2010.
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derived DNA SEQ ID 151
                                                                                                                        5635 AA.
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                                                                                                                                                                                                                                              512 AA
                                     Score
Pred.
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Pred.
                                                                                                                                                          Score 154.5; DB 6; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                     Score 154.5; DB 8; Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154.5; DB 8; Pred. No. 0.00017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 156.5; DB 6
Pred. No. 0.00014;
                                     154.5; DB
No. 0.0086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156; DB 4;
No. 0.00035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373;
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Query Match
Best Local Similarity
RESULT 1155
                                                                                                                                                        RESULT 1154
                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  RESULT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1151
                                                                                                                                                                                                                                                                                                                                                             Query
Best I
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                         Query Match
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                       Sequence gi/1017427/emb/CAA62189
WO9960164-A1.
                                                                                                                                                                                                                                                                                                           Angiogenesis differentially FR2836687-A1.
                                                                                                                         ADP73129 standard; protein; 5636 AA. Angiogenesis inhibitor human protein FR2843753-A1.
                                                                                                                                                                                                                      ADK60506 standard; protein; Angiogenesis differentially FR2836686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BUCK-) BUCK INST AGE RES.
PRY Match 7.4%;
T Local Similarity 23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003087768-A2
23-OCT-2003.
                                                                                                                                                                                      (GENE-) GENE SIGNAL. (ALMA/) AL MAHMOOD S.
                                                                                                                                                                                                                                                                                   (GENE-) GENE SIGNAL. (ALMA/) AL MAHMOOD S
          25-NOV-1999
(QUAR-) QUA
                                                                                        (GENE/) GENE S.
(ALMS/) AL M S.
                                                                                                                 27-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human hemicentin
US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ83137 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                   (SMIT/)
                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
  Match
                                                                                                                                                                                                                                                                                                                                                                             ) MILLET I.
) SCIORE P.
) ELLERMAN K.
) MACDOUGALL J R
) SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FERNANDES E R
RIEGER D K.
EDINGER S R.
GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
         QUARK BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSOBROOK J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                     Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽.
                                                                                                                                                                 7.4%;
23.4%;
                                                                                                                                                                                                                                                              7.4%;
23.4%;
                                                                                                                                                                                                                                                                                                                                                           7.4%;
23.4%;
                                                                                                                                                                                                                                                                                                                                                                                            ₽.
                                                                       23
INC.
7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 5636 AA.
SEQ ID 128.
                                                                                                                                                                                                                                5636 AA.
                                                                                                                                                                                                                                                                                                                             5636 AA.
expressed
                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                               Score
Pred.
                                                                       Score
Pred.
                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                            Score 154.5; DB 7; Pred. No. 0.0086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
 Score 153.5;
                                        AA.
from
                                                                       154
No.
                                                                                                                                                                   154
No.
                                                                                                                                                                                                                                                              154.5; DB
No. 0.0086;
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No. 0.0086;
                                                                                                                                    sequence,
                                        an
                                                                        0.0086;
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                                                                                                                                                                                                                                 protein GS-P29
                                                                                                                                                                                                                                                                                                                             protein GS-P29
                                        alignment
 DΒ
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 Length 4412;
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                                        with
                                        protein
                                                                                                                                                                              5636;
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Best Local Similarity
RESULT 1156
ID ADA50158 standard; p
DE Human CAR/mouse SCF
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
RESULT 1157
 PA PA PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1158
                                                                        RESULT
                                                                                                                                                                                                                                                Best Local Similarity RESULT 1161
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1159
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunoglobulin polypeptide SEQ WO200155315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ITOH/) ITOH A.
(HANA/) HANAZONO Y.
(OKAD/) OKADA T.
(OZAW/) OZAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ITOH/) ITOH A.
(HANA/) HANAZONO Y.
(OKAD/) OKADA T.
(OZAW/) OZAWA K.
                                                                                                                            ADR41522 standard; protein; 318 Human CD-like molecule HKACI03, WO200226930-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CAR/mouse SCF
US2003092068-A1.
15-MAY-2003.
                                         ADA50157 standard; protein; Human CAR/SCF mature fusion US2003092068-A1.
                                                                                                                                                                                                               Human novel protein US2003077606-A1.
                                                                                                                                                                                                                                                                                                                       ABP66819 standard;
Human polypeptide 9
US2002090672-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           ABB10232 standard; protein; 301 Human cDNA SEQ ID NO: 540. WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA50159 standard; protein; 474 AA. Human CAR/mouse anti-CD34 antibody US2003092068-A1.
                                                                                                                                                                                                        24-APR-2003
                                                                                                         (HUMA-) HUMAN
                                                                                                                                                                                                                                      ADB31620 standard;
                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC. ry Match 7.2%; Local Similarity 25.8%;
                                                                                                                                                                                           HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                         ROSE/) ROSEN C A. RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                              BARA/) BARASH S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                       Local Similarity
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                                                                                   Local Similarity
HANAZONO Y.
OKADA T.
                     ITOH A.
                                                                                                GENOME SCI INC.
7.2%;
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                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                         protein;
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                                                                                                                                                                       7.2%;
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25.8%;
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23.2%;
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24.3%;
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                                                                                                                                                                                                                           ; 301 AA.
NO 141.
                                                                                                                                                                                                                                                                                                                                   301 AA.
540.
                                                   393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion protein
                                                                                Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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No. (
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No. 0.
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No.
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No. 0.00041;
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No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      151; DB 4;
No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mature
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                                                                                                                                         NO:321
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                                                                                    DB 5;
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.00026;
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                                                                                            Length
                                                                                                                                                                                                                                                                   Length 301;
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Best Local Similarity
RESULT 1172
ID AAPPOOL
                                                                                                    Best Local Similarity RESULT 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA (REGC) UNIV CALIFORNIA.
Query Match 7.1%;
Best Local Similarity 20.5%;
RESULT 1167
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RESULT 1166
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Best Local Similarity
RESULT 1164
                                                                                                                                                                                              Best Local Similarity RESULT 1170
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RESULT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1168
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                                                                  AAB48126 standard; prot
Mouse A236 polypeptide.
WO200069885-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU62399 standard; protein; 466 AA. Chimeric CAR/Hg/Pro-A gene product. US6524572-B1.
                                                                                                                                                 ABB68257 standard; protein; Drosophila melanogaster poly WO200171042-A2.
                                                                                                                                                                                                                                                                AAB85862 standard; protein; Murine adipocytes-derived pw0200166720-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADB85335 standard; protein; 1395 AA.
Fruitfly nerve cell growth modulator SLIT-1-associated sequence US2003170727-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1999.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY13563 standard; protein; 1395
Drosophila Robo 1 polypeptde.
W09925833-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OZAW/) OZAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila sp. WO9920764-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY08401 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2.
11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG02117 standard; protein; 434 AA. Novel human diagnostic protein #2108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG02117 standard;
                                            23-NOV-2000.
(MILL-) MILLENNIUM
                                                                                                                                                                                                                              (KITA/) KITAMURA T.
(TSUR/) TSURUGA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RAIN-) RAINBOW THERAPEUTIC CO.
ry Match 7.2%; Score
t Local Similarity 25.4%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2003.
                                                                                                                                      PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                              KIDD T.
BROSE K.
                                                                                                                                                                                                                                                                                                            TESSIER-LAVIGNE M.
7.1%;
Similarity 20.5%;
                                                                                                                                                                                                                                                                                                                                                                    GOODMAN C S.
standard; protein; 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROBO1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                       7.1%;
                                   PHARM INC.
7.1%;
                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                     7.1%;
21.7%;
                                                                                                                7.1%;
20.2%;
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21.7%;
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24.3%;
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25.4%;
                                                                                                                                                                     ein; 1395 AA
polypeptide
                                                                                                                                                                                                                                                                           n; 373 AA.
l protein.
                                                                                           373
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                      Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. (
                                                                                                                                                                                                          Score 149;
Pred. No. (
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Pred. No. 0.
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Pred. No. 0.
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                      148;
No. 0.
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No. (
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0.00049;
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                       DB 4;
.00064;
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.00053;
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.00044;
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Mouse A236 protein. US2002055139-A1.

A236

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(HYSE-)
Query Match
Best Local
RESULT 1
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Best I
RESULT 1
                                                                                                                                            Query Matc
Best Local
RESULT 1178
ID AAB4814
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Best I
RESULT 1
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Best Local Similarity
RESULT 1175
                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1176
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Best Local Similarity
RESULT 1173
                                                                                                                                                                                                                                                                                                                                                                                                      Human OCP protein #6.
US2004053301-A1.
18-MAR-2004
                                                                                                                                                                                                                                                                   AAB48149 standard;
Mouse A236 variant
WO200069885 A2.
                                                                                                                          AAB48148 standard;
Mouse A236 variant
WO200069885-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicted human adlican-2
WO200246364-A2.
                                                     ABG22401 standard; protein; 361 AA.
Novel human diagnostic protein #22392.
W0200175067-A2.
   ABB66424 standard;
                                                                                                                                                                            23-NOV-2000.
                                                                                                                                                                                               WO200069885-A2.
                                                                                                                                                                                                        Mouse A236 variant
                                                                                                                                                                                                                AB48150 standard;
                                                                                                                                                                                                                                                                                                                                                          ABP70049 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (QUAR-) QUARK BIOTECH INC.
ry Match 7.0%;
Local Similarity 21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG31321 standard; protein;
                                                                                                          (MILL-) MILLENNIUM
                                                                                                                                                                                                                                                   MILL-) MILLENNIUM
                                                                                                                                                                                                                                                                                                                         CURA-) CURAGEN
                                                                                                                                                                                                                                                                                                                                                                                            QUAR-) QUARK BIOTECH
                                                                                μοcal Similarity
1179
            Local Similarity
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) BARNES T M.
) FRASER C C.
) WRIGHTON N.
) MYERS P S.
) KINGSBURY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHARP J D.
LEIBY K R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOSSONE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOLTZMAN
                                     INC.
                                                                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DA.
                                                                                                                                                           7.0%;
21.3%;
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3 polypep
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2 polypeptide.
                                                                                                                                 protein; 373 A
1 polypeptide.
                                                                                                                                                                                                                                           PHARM INC. 7.0%;
   protein;
                                                                                                          PHARM INC.
                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                           CH INC.
7.0%;
21.8%;
                                                                                       7.0%;
21.7%;
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21.7%;
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21.8%;
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21.7%;
                    7.0%;
24.5%;
                                                                                                                                                                                                     rotein; 373 AA.
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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    2016 AA
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Pred.
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Pred.
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                          Mouse brain immu
WO200129083-A1.
26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                ADE08316 standard; protein; 538 AA.

Novel protein (useful for identifying genetic w02003054152-A2.
                                                                                                              AAY69287 standard; |
Amino acid sequence
WO200008057-A2.
                                                                                                                                                                                                                                                                            Drosophila melanogaster WO200171042-A2.
27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neurotrimin WO2003002765-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ89652 standard;
Antagonist of cell
WO2004063362-A2.
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Drosophila melanog;
WO200171042-A2.
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Murine nectin-like
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(HYSE-) HYSEQ INC.
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                                                        AAE00868 standard;
                                                                                           (IMMV ) IMMUNEX CORP.
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                   (TEXA-)
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                                                                                                                                                                      (LARR/) LARRICK J W
(WYCO/) WYCOFF K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYCL-) CYCLACEL LTD.
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h 6.9%; Score 144; DB 7;
Similarity 26.6%; Pred. No. 0.0014;
                  TEXAS BIOTECHNOLOGY CORP
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progression
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superfamily
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                                Mouse coxsackievirus and ade Mo9811221-A2.
                                                                                                                                                                                          Mouse coxsackievirus and Ad: WO9833819-A1.
                                                                                                                      ABB63920 standard; protein; Drosophila melanogaster poly WO200171042-A2.
                                                                                                                                                                                                                                                                  ABB71502 standard; protein; 1052 AA. Drosophila melanogaster polypeptide SEQ WO200171042-A2.
27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                     ABO84469 standard; protein; 3475 AA. Human cancer-associated protein HP13-036.1. WO2004074320-A2.
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Human heat mitochondrial protein as
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Mouse protein SEQ
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23-OCT-2003.
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ry Match 6.7%;
t Local Similarity 25.4%;
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(NUVE-) NUVELO INC.
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Novel human diagnostic protein
W0200175067-A2.
11-OCT-2001.
(HYSEQ INC.
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Human platelet deri
US2002111304-A1.
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US2002111304-A1.
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                           Platelet de
EP325224-A.
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EP1201681-A1.
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JP2004208583-A.
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WO200029582-*~
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          OMYZ)
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(IKUN/) IKUNO Y.
                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
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                                                                                  IKUN/) IKUNO
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15-AUG-2002.
(KAZL/) KAZLAUSKAS /
(IKUN/) IKUNO Y.
                                                                                                                                                                                                                                                             ABG72458 standard; protein; 1106 AA. Human platelet derived growth factor US2002111304-A1.
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Human platelet derived growth factor receptor beta mutant E594K.
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                                                                         WO2003070083-A2.
28-AUG-2003.
                                                                                          ABR84719 standard; protein; 1106 AA.
Human PDGF beta receptor protein.
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EP721983-A1.
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IKUN/) IKUNO Y.
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(IKUN/) IKUNO Y.
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PA (SUNE-) SUNESIS PHARM INC.
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RESULT 1215
ID ADF45082 standard;
DE Human kinase PDGFR-
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05-SEP-2001.

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                   Human PRO1868 polypeptide WO200140466-A2.
07-JUN-2001.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                   Human PRO1868 protein, WOZ00104311-A1.
                                                             AAU12440 standard;
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Human polypeptide,
EP1130094-A2.
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ixy Match

t Local Similarity 21.8%;
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Human polypeptide,
EP1130094-A2.
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Human confluency regulated adhesion molecule 1
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Human PRO1868 protein UNQ859
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ry Match 6.6%;
Local Similarity 21.8%;
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(SAGR-) SAGRES DISCOVERY INC.
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SEQ ID NO: 2845.
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                                  Human albumin fusion protein #19
WO200177137-A1.
                                                                                                                      Human albumin fusion protein #1971. W0200177137-A1.
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                    (HUMA-) HUMAN GENOME SCI INC.
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c Local Similarity 21.8%;
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(GETH ) GENENTECH INC.
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Query Match
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RESULT 1238
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RESULT 1236
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RESULT 1237
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(GETTU )
                                                            Human PRO polypeptide #61. US2002192659-A1.
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Human secreted and
US2002192668-A1.
ADA57610 standard; protein;
Human secreted protein #592
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Human PRO polypeptide #61.
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WO200208284-A2.
31-JAN-2002.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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ID AB047422 standard; p
DE Human secreted/trans
PN US2003044839-A1.
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Best Local Similarity
RESULT 1248
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Human PRO pdlypeptide #269.
US2003004311-A1.
02-JAN-2003;
(GETH) GENENTECH INC.
                                                                                                                                                              Human PRO polypeptide #269.
US2003036180-A1.
20-FEB-2007
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                                                                                             ABU54407 standard; protein; 310 AA. Human secreted/transmembrane protein
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(TEXA) 6.6%; Score
ry Match 6.6%; Pred.
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27-DEC-2002.
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ry Match 6.6%;
t Local Similarity 21.8%;
           ABO47422 standard; protein; 310 AA.
Human secreted/transmembrane polypo
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Best Local Similarity
RESULT 1250
ID ARCTON
Query Match
Best Local Similarity
RESULT 1258
ID ABU81236 standard; p
DE Human PRO1917polypep
PN US2003032060-A1.
PD 13-FEB-2003.
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RESULT 1257
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RESULT 1256
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         ABU81236 standard; protei
Human PRO1917polypeptide.
US2003032060-A1.
                                                                                   ABU67114 standard; protein; 310 AA. Human secreted/transmembrane, PRO, US2003032155-A1.
                                                                                                                                                              ABU60813 standard; protein; : Human secreted/transmembrane US2002160392-A1.
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20-FEB-2003.
(GETH ) GENENTECH INC.
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US2003023054-A1.
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Novel secreted and
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(GETH) GENENTECH
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(GETH ) GENENTECH INC.
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Query Match
Best Local Similarity
RESULT 1267
ID ADB28087 standard; p
DE Human PRO polypeptid
PN US2003082704-A1.
PD 01-MAY-2003
PA (GETH) GENENTECH IN
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     Human PRO polypeptide #269. US2003082704-Al. 01-MAY-2003.
                                                                                          Novel human secreted and transmembr. US2003068796-Al.
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US2003049816-A1.
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Human PRO polypeptide #269.
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23-JAN-2003.
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GENERTECH INC

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US2003082711-A1.
                  ....ard; protein;
US2003082705-A1.
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Human secreted/transmembrane
US2003039971-A1.
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Human PRO polypeptide #269.
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08-MAY-2003.
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17-APR-2003.
IGETH) GENENTECH INC.
                              Human PRO polypeptide #269. US2003077722-A1. 24-APR-2003
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Human PRO polypeptide #269.
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Novel human secreted and tra
US2003082694-A1.
01-MAY-2003.
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06-MAR-2003.
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US2003087345-A1.
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Human PRO polypeptide #61.
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Human PRO polypeptide SEQ ID NO
US2003077715-A1.
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Human PRO polypeptide #269.
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Human secreted/transmembrane 
US2003039969-A1.
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Novel human secreted and tra
US2003082709 -A1.
01-MAY-2003.
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Human secreted/transmembrane
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ADA43030 standard; protein; Human secreted/transmembrane US2003054351-A1.
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US2003027256-A1.
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US2003082686-A1.
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US2003073213-A1.
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                                            ADB89830 standard; protein; Human PRO polypeptide #269.
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Human PRO polypeptide #269.
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                                                                                                                                                                                                                                                                          ADC19269 standard; protein; 310 AA. Human secreted/transmembrane protein, US2003036061-A1.
20-FEB-2003.
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                                                                                                                           ADC34569 standard; protein; Human secreted/transmembrane US2003036094-A1.
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20-MAR-2003.
(GETH) GENENTECH INC.
                                                                                                                                                  ADC50579 standard;
Novel human secrete
                                                                                                                                                                                                                                                                                            ADC13215 standard; protein; Human secreted/transmembrane US2003073079-A1.
                                                                                                                                                                                                                                                                                                                                                                      ADC34145 standard; protein; Human secreted/transmembrane US2003073077-A1.
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                                                                                                                                                                                                                            Human PRO1868 protein.
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                                                                                                                                                                                                                                       AAE38826 standard;
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ADC56119 standard;
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ADC48663 standard; protein;
Human PRO polypeptide #269.
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US2003087358-Al.
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Human PRO polypeptide #269.
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Human secreted/transmembrane PRO
US2003105012-A1.
05-JUN-2003.
(GETH.) GENENTECH INC.
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                                                                                                          ADD91568 standard; protein;
Human PRO polypeptide #269.
US2003199055-A1.
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Human PRO polypeptide #269.
US2003199030-A1.
23-OCT-2003.
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Human PRO polypeptide #269.
US2003203431-A1.
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(GETH) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #269.
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Novel human secreted and transmembrane
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PD 06-NOV-2003.
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27-FEB-2003.
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Human PRO polypeptide #269.
US2003207372-A1.
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US2003207377-A1.
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US2003207387-A1.
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US2003170864-A1.
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US2003087353-A1.
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Novel human secreted and tran.
US20030877357-Al.
08-MAY-2003.
(GETH ) GENENTECH INC.
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                                    ADE73601 standard; protein; Human secreted/transmembrane U62003129592-A1.
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US2003211571-A1.
19-007-2003.
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Human PRO polypeptide #269.
US2003203440-Al.
30-OCT-2003.
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Human PRO polypeptide #269.
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Human secreted/transmembrane
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US2003092108-A1.
15-MAY-2003.
(GETH ) GENENTECH TWO
              Human PRO polypeptide #269.
US2003199054-A1.
23-OCT-2003.
(GETH ) GENENTFOU TWO
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US2003194794-A1.
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Human PRO polypeptide #269.
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ADG24433 standard; protein; 310 AA. Novel human secreted and transmembrane US2003207426-A1.
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Human PRO polypeptide #269.
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US2003207360-A1.
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US2003208055-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #269.
US2003207425-A1.
06-NOV-2003.
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